Clone UNQ230 (DNA34431-1177) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209399.

Analysis of the amino acid sequence of the full-length PRO263 polypeptide suggests that portions of it possess significant homology to CD44 antigen, thereby indicating that PRO263 may be a novel cell surface adhesion molecule.

EXAMPLE 34: Isolation of cDNA Clones Encoding Human PRO270

A consensus DNA sequence was assembled relative to the other identified EST sequences as described in Example 1 above, wherein the consensus sequence was designated herein as DNA35712. Based on the DNA35712 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO270.

Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-GCTTGGATATTCGCATGGGCCTAC-3' (SEQ ID NO:208)

forward PCR primer (.f2) 5'-TGGAGACAATATCCCTGAGG-3' (SEQ ID NO:209)

reverse PCR primer (.r1) 5'-AACAGTTGGCCACAGCATGGCAGG-3' (SEQ ID NO:210)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35712 sequence which had the following nucleotide sequence

hybridization probe

5'-CCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAG-3' (SEQ ID NO:211)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO270 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO270 [herein designated as UNQ237, DNA39510-1181] (SEQ ID NO:206) and the derived protein sequence for PRO270.

The entire nucleotide sequence of UNQ237, DNA39510-1181 is shown in Figure 75 (SEQ ID NO:206). Clone UNQ237 (DNA39510-1181) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 3-5 and ending at the stop codon at nucleotide positions 891-893 (Fig. 75; SEQ ID NO:206). The predicted polypeptide precursor is 296 amino acids long (Fig. 76). Clone UNQ237 (DNA39510-1181) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209392.

Analysis of the amino acid sequence of the full-length PRO270 suggests that portions of it possess significant homology to the thioredoxin-protein, thereby indicating that the PRO270 protein may be a novel member of the thioredoxin family.

EXAMPLE 35: Isolation of cDNA Clones Encoding Human PRO271

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35737. Based on the DNA35737 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of

interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO271.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-TGCTTCGCTACTGCCCTC-3' (SEQ ID NO:214)
forward PCR primer 2 5'-TTCCCTTGTGGGTTGGAG-3' (SEQ ID NO:215)
forward PCR primer 3 5'-AGGGCTGGAAGCCAGTTC-3' (SEQ ID NO:216)
reverse PCR primer 1 5'-AGCCAGTGAGGAAATGCG-3' (SEQ ID NO:217)
reverse PCR primer 2 5'-TGTCCAAAGTACACACACCTGAGG-3' (SEQ ID NO:218)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35737 sequence which had the following nucleotide sequence

hybridization probe

5'-GATGCCACGATCGCCAAGGTGGGACAGCTCTTTGCCGCCTGGAAG-3' (SEQ ID NO:219)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO271 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO271 [herein designated as UNQ238 (DNA39423-1182)] (SEQ ID NO:212) and the derived protein sequence for PRO271.

The entire nucleotide sequence of UNQ238 (DNA39423-1182) is shown in Figure 77 (SEQ ID NO:212). Clone UNQ238 (DNA39423-1182) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 101-103 and ending at the stop codon at nucleotide positions 1181-1183 (Figure 77). The predicted polypeptide precursor is 360 amino acids long (Figure 78). Clone UNQ238 (DNA39423-1182) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209387.

Analysis of the amino acid sequence of the full-length PRO271 polypeptide suggests that it possess significant homology to the proteoglycan link protein, thereby indicating that PRO271 may be a link protein homolog.

EXAMPLE 36: Isolation of cDNA Clones Encoding Human PRO272

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example I above. This consensus sequence is herein designated DNA36460. Based on the DNA36460 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO272.

Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-CGCAGGCCCTCATGGCCAGG-3' (SEQ ID NO:222)
forward PCR primer (.f2) 5'-GAAATCCTGGGTAATTGG-3' (SEQ ID NO:223)
reverse PCR primer 5'-GTGCGCGGTGCTCACAGCTCATC-3' (SEQ ID NO:224)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA36460 sequence which had the following nucleotide sequence

hybridization probe

5'-CCCCCCTGAGCGACGCTCCCCCATGATGACGCCCACGGGAACTTC-3' (SEQ ID NO:225)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO272 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO272 [herein designated as UNQ239 (DNA40620-1183)] (SEQ ID NO:220) and the derived protein sequence for PRO272.

The entire nucleotide sequence of UNQ239 (DNA40620-1183) is shown in Figure 79 (SEQ ID NO:220). Clone UNQ239 (DNA40620-1183) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 35-37 and ending at the stop codon at nucleotide positions 1019-1021 (Figure 79). The predicted polypeptide precursor is 328 amino acids long (Figure 80). Clone UNQ239 (DNA40620-1183) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209388.

Analysis of the amino acid sequence of the full-length PRO272 polypeptide suggests that portions of it possess significant homology to the human and mouse reticulocalbin proteins, respectively, thereby indicating that PRO272 may be a novel reticulocalbin protein.

EXAMPLE 37: Isolation of cDNA Clones Encoding Human PRO294

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35731. Based on the DNA35731 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO294.

Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-TGGTCTCGCACACCGATC-3' (SEQ ID NO:228)
forward PCR primer (.f2) 5'-CTGCTGTCCACAGGGGAG-3' (SEQ ID NO:229)
forward PCR primer (.f3) 5'-CCTTGAAGCATACTGCTC-3' (SEQ ID NO:230)
forward PCR primer (.f4) 5'-GAGATAGCAATTTCCGCC-3' (SEQ ID NO:231)
reverse PCR primer (.r1) 5'-TTCCTCAAGAGGGCAGCC-3' (SEQ ID NO:232)
reverse PCR primer (.r2) 5'-CTTGGCACCAATGTCCGAGATTTC-3' (SEQ ID NO:233)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35731 sequence which had the following nucleotide sequence

hybridization probe
5'-GCTCTGAGGAAGGTGACGCGCGGGGCCTCCGAACCCTTGGCCTTG-3' (SEQ ID NO:234)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO294 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO294 [herein designated as

UNQ257 (DNA40604-1187)] (SEQ ID NO:226) and the derived protein sequence for PRO294.

The entire nucleotide sequence of UNQ257 (DNA40604-1187) is shown in Figure 81 (SEQ ID NO:226). Clone UNQ257 (DNA40604-1187) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 396-398 and ending at the stop codon at nucleotide positions 2046-2048 (Figure 81). The predicted polypeptide precursor is 550 amino acids long (Figure 82). Clone UNQ257 (DNA40604-1187) has been deposited with ATCC and is assigned ATCC deposit no. 209394.

Analysis of the amino acid sequence of the full-length PRO294 polypeptide suggests that portions of it possess significant homology to portions of various collagen proteins, thereby indicating that PRO294 may be collagen-like molecule.

EXAMPLE 38: Isolation of cDNA Clones Encoding Human PRO295

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35814. Based on the DNA35814 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO295.

Forward and reverse PCR primers were synthesized:

forward PCR primer (.f1) 5'-GCAGAGCGGAGATGCAGCGGCTTG-3' (SEQ ID NO:238)

forward PCR primer (.f2) 5'-CCCAGCATGTACTGCCAG-3' (SEQ ID NO:239)

forward PCR primer (.f3) 5'-TTGGCAGCTTCATGGAGG-3' (SEQ ID NO:240)

forward PCR primer (.f4) 5'-CCTGGGCAAAAATGCAAC-3' (SEQ ID NO:241)

reverse PCR primer (.r1) 5'-CTCCAGCTCCTGGCGCACCTCCTC-3' (SEQ ID NO:242)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35814 sequence which had the following nucleotide sequence

hybridization probe

5'-GGCTCTCAGCTACCGCGCAGGAGCGAGGCCACCCTCAATGAGATG-3' (SEQ ID NO:243)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO295 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO295 [herein designated as UNQ258 (DNA38268-1188)] (SEQ ID NO:235) and the derived protein sequence for PRO295.

The entire nucleotide sequence of UNQ258 (DNA38268-1188) is shown in Figure 83 (SEQ ID NO:235). Clone UNQ258 (DNA38268-1188) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 153-155 and ending at the stop codon at nucleotide positions 1202-1204 (Figure 83). The predicted polypeptide precursor is 350 amino acids long (Figure 84). Clone UNQ258 (DNA38268-1188) has been deposited with ATCC and is assigned ATCC deposit no. 209421.

Analysis of the amino acid sequence of the full-length PRO295 polypeptide suggests that portions of it possess significant homology to the integrin proteins, thereby indicating that PRO295 may be a novel integrin.

EXAMPLE 39: Isolation of cDNA Clones Encoding Human PRO293

The extracellular domain (ECD) sequences (including the secretion signal, if any) of from about 950 known secreted proteins from the Swiss-Prot public protein database were used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altshul et al., Methods in Enzymology 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequence. Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington; http://bozeman.mbt.washington.edu/phrap.docs/phrap.html).

Based on an expression tag sequence designated herein as T08294 identified in the above analysis, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO293.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AACAAGGTAAGATGCCATCCTG-3' (SEQ ID NO:246)

reverse PCR primer 5'-AAACTTGTCGATGGAGACCAGCTC-3' (SEQ ID NO:247)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the expression sequence tag which had the following nucleotide sequence

hybridization probe

5'-AGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGC-3' (SEQ ID NO:248)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO293 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO293 [herein designated as UNQ256 (DNA37151-1193)] (SEQ ID NO:244) and the derived protein sequence for PRO293.

The entire nucleotide sequence of UNQ256 (DNA37151-1193) is shown in Figures 85A-B (SEQ ID NO:244). Clone UNQ256 (DNA37151-1193) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 881-883 and ending at the stop codon after nucleotide position 3019 of SEQ ID NO:244, Figures 85A-B). The predicted polypeptide precursor is 713 amino acids long (Figure 86). Clone UNQ256 (DNA37151-1193) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209393.

Analysis of the amino acid sequence of the full-length PRO293 polypeptide suggests that portions of it possess significant homology to the NLRR proteins, thereby indicating that PRO293 may be a novel NLRR protein.

EXAMPLE 40: Isolation of cDNA Clones Encoding Human PRO247

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA33480. Based on the DNA33480 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO247.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAACAATGAGGGCACCAAGC-3' (SEQ ID NO:251)

reverse PCR primer 5'-GATGGCTAGGTTCTGGAGGTTCTG-3' (SEQ ID NO:252)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA33480 expression sequence tag which had the following nucleotide sequence

hybridization probe

5'-CAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCG-3' (SEQ ID NO:253)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO247 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO247 [herein designated as UNQ221 (DNA35673-1201)] (SEQ ID NO:249) and the derived protein sequence for PRO247.

The entire nucleotide sequence of UNQ221 (DNA35673-1201) is shown in Figures 89A-B (SEQ ID NO:249). Clone UNQ221 (DNA35673-1201) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 80-82 of SEQ ID NO:249 and ending at the stop codon after nucleotide position 1717 of SEQ ID NO:249 (Figures 89A-B). The predicted polypeptide precursor is 546 amino acids long (Figure 88). Clone UNQ221 (DNA35673-1201) has been deposited with ATCC and is assigned ATCC deposit no. 209418.

Analysis of the amino acid sequence of the full-length PRO247 polypeptide suggests that portions of it possess significant homology to the densin molecule and KIAA0231, thereby indicating that PRO247 may be a novel leucine rich repeat protein.

EXAMPLE 41: Isolation of cDNA Clones Encoding Human PRO302, PRO303, PRO304, PRO307 and PRO343

Consensus DNA sequences were assembled relative to other EST sequences using phrap as described in Example 1 above. These consensus sequences are herein designated DNA35953, DNA35955, DNA35958, DNA37160 and DNA30895. Based on the DNA35953 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO302.

PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GTCCGCAAGGATGCCTACATGTTC-3' (SEQ ID NO:264)

forward PCR primer 2 5'-GCAGAGGTGTCTAAGGTTG-3' (SEQ ID NO:265)

reverse PCR primer 5'-AGCTCTAGACCAATGCCAGCTTCC-3' (SEQ ID NO:266)

Also, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35953 sequence which had the following nucleotide sequence

hybridization probe

5'-GCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATG-3' (SEQ ID NO:267)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO302 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB228).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO302 [herein designated as UNQ265 (DNA40370-1217)] (SEQ ID NO:254) and the derived protein sequence for PRO302.

The entire nucleotide sequence of UNQ265 (DNA40370-1217) is shown in Figure 89 (SEQ ID NO:254). Clone UNQ265 (DNA40370-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 34-36 and ending at the stop codon at nucleotide positions 1390-1392 (Figure 89). The predicted polypeptide precursor is 452 amino acids long (Figure 90). Various unique aspects of the PRO302 protein are shown in Figure 90. Clone UNQ265 (DNA40370-1217) has been deposited with the ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209485.

Based on the DNA35955 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO303.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGGGAATTCACCCTATGACATTGCC-3' (SEQ ID NO:268)

reverse PCR primer 5'-GAATGCCCTGCAAGCATCAACTGG-3' (SEQ ID NO:269)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35955 sequence which had the following nucleotide sequence:

hybridization probe

5'-GCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAGGCCTC-3' (SEQ ID NO:270)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO303 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO303 [herein designated as UNQ266 (DNA42551-1217)] (SEQ ID NO:256) and the derived protein sequence for PRO303.

The entire nucleotide sequence of UNQ266 (DNA42551-1217) is shown in Figure 91 (SEQ ID NO:256). Clone UNQ266 (DNA42551-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 20-22 and ending at the stop codon at nucleotide positions 962-964 (Figure 91). The predicted polypeptide precursor is 314 amino acids long (Figure 92). Various unique aspects of the PRO303 protein are shown in Figure 92. Clone UNQ266 (DNA42551-1217) has been deposited on November 21, 1997 with the ATCC and is assigned ATCC deposit no. ATCC 209483.

Based on the DNA35958 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO304.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GCGGAAGGGCAGAATGGGACTCCAAG-3' (SEQ ID NO:271)
forward PCR primer 2 5'-CAGCCCTGCCACATGTGC-3' (SEQ ID NO:272)
forward PCR primer 3 5'-TACTGGGTGGTCAGCAAC-3' (SEQ ID NO:273)
reverse PCR primer 5'-GGCGAAGAGCAGGGTGAGACCCCG-3' (SEQ ID NO:274)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35958 sequence which had the following nucleotide sequence

hybridization probe
5'-GCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGAC-3' (SEQ ID NO:275)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO304 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from 22 week human fetal brain tissue (LIB153).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO304 [herein designated as UNQ267 (DNA39520-1217)] (SEQ ID NO:258) and the derived protein sequence for PRO304.

The entire nucleotide sequence of UNQ267 (DNA39520-1217) is shown in Figure 93 (SEQ ID NO:258). Clone UNQ267 (DNA39520-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 34-36 and ending at the stop codon at nucleotide positions 1702-1704 (Figure 93). The predicted polypeptide precursor is 556 amino acids long (Figure 94). Various unique aspects of the PRO304 protein are shown in Figure 94. Clone UNQ267 (DNA39520-1217) has been deposited with ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209482.

Based on the DNA37160 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO307.

Pairs of PCR primers (forward and reverse) were synthesized:

forward PCR primer 1 5'-GGGCAGGGATTCCAGGGCTCC-3' (SEQ ID NO:276)
forward PCR primer 2 5'-GGCTATGACAGCAGGTTC-3' (SEQ ID NO:277)
forward PCR primer 3 5'-TGACAATGACCGACCAGG-3' (SEQ ID NO:278)
reverse PCR primer 5'-GCATCGCATTGCTGGTAGAGCAAG-3' (SEQ ID NO:279)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA37160 sequence which had the following nucleotide sequence

hybridization probe
5'-TTACAGTGCCCCCTGGAAACCCACTTGGCCTGCATACCGCCTCCC-3' (SEQ ID NO:280)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones

encoding the PRO307 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO307 [herein designated as UNQ270 (DNA41225-1217)] (SEQ ID NO:260) and the derived protein sequence for PRO307.

The entire nucleotide sequence of UNQ270 (DNA41225-1217) is shown in Figure 95 (SEQ ID NO:260). Clone UNQ270 (DNA41225-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 92-94 and ending at the stop codon at nucleotide positions 1241-1243 (Figure 95). The predicted polypeptide precursor is 383 amino acids long (Figure 96). Various unique aspects of the PRO307 protein are shown in Figure 96. Clone UNQ270 (DNA41225-1217) has been deposited with ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209491.

Based on the DNA30895 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO343.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CGTCTCGAGCGCTCCATACAGTTCCCTTGCCCCA-3' (SEQ ID NO:281)

reverse PCR primer

5'-TGGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCC
CCCTCATGTGCCAGGTGGA-3' (SEQ ID NO:282)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA30895 sequence which had the following nucleotide sequence

hybridization probe

5'-CCCTCAGACCCTGCAGAAGCTGAAGGTTCCTATCATCGAC
TCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGT
GTGCCGGCTACT-3' (SEQ ID NO:283)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO343 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB26).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO343 [herein designated as UNQ302 (DNA43318-1217)] (SEQ ID NO:262) and the derived protein sequence for PRO343.

The entire nucleotide sequence of UNQ302 (DNA43318-1217) is shown in Figure 97 (SEQ ID NO:262). Clone UNQ302 (DNA43318-1217) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 53-55 and ending at the stop codon at nucleotide positions 1004-1006 (Figure 97). The predicted polypeptide precursor is 317 amino acids long (Figure 98). Various unique aspects of the PRO343 protein are shown in Figure 98. Clone UNQ302 (DNA43318-1217) has been deposited with ATCC on November 21, 1997 and is assigned ATCC deposit no. ATCC 209481.

EXAMPLE 42: Isolation of cDNA Clones Encoding Human PRO328

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35615. Based on the DNA35615 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO328.

Forward and reverse PCR primers were synthesized:

forward PCR primer 5'-TCCTGCAGTTTCCTGATGC-3' (SEQ ID NO:286)

reverse PCR primer 5'-CTCATATTGCACACCAGTAATTCG-3' (SEQ ID NO:287)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35615 sequence which had the following nucleotide sequence

hybridization probe

5'-ATGAGGAGAAACGTTTGATGGTGGAGCTGCACAACCTCTACCGGG-3' (SEQ ID NO:288)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO328 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO328 [herein designated as UNQ289 (DNA40587-1231)] (SEQ ID NO:284) and the derived protein sequence for PRO328.

The entire nucleotide sequence of UNQ289 (DNA40587-1231) is shown in Figure 99 (SEQ ID NO:284). Clone UNQ289 (DNA40587-1231) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 15-17 and ending at the stop codon at nucleotide positions 1404-1406 (Figure 99). The predicted polypeptide precursor is 463 amino acids long (Figure 100). Clone UNQ289 (DNA40587-1231) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209438.

Analysis of the amino acid sequence of the full-length PRO328 polypeptide suggests that portions of it possess significant homology to the human glioblastoma protein and to the cysteine rich secretory protein thereby indicating that PRO328 may be a novel glioblastoma protein or cysteine rich secretory protein.

EXAMPLE 43: Isolation of cDNA Clones Encoding Human PRO335, PRO331 or PRO326

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA36685. Based on the DNA36685 consensus sequence, and Incyte EST sequence no. 2228990, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO335, PRO331 or PRO326.

Forward and reverse PCR primers were synthesized for the determination of PRO335:

forward PCR primer 5'-GGAACCGAATCTCAGCTA-3' (SEQ ID NO:295)

forward PCR primer 5'-CCTAAACTGAACTGGACCA-3' (SEQ ID NO:296)

forward PCR primer 5'-GGCTGGAGACACTGAACCT-3' (SEQ ID NO:297)

forward PCR primer: 5'-ACAGCTGCACAGCTCAGAACAGTG-3' (SEQ ID NO:298)

reverse PCR primer 5'-CATTCCCAGTATAAAAATTTTC-3' (SEQ ID NO:299)

reverse PCR primer 5'-GGGTCTTGGTGAATGAGG-3' (SEQ ID NO:300)

reverse PCR primer 5'-GTGCCTCTCGGTTACCACCAATGG-3' (SEQ ID NO:301)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO335 which had the following nucleotide sequence

hybridization probe

5'-GCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTAC-3'

(SEQ ID NO:302)

Forward and reverse PCR primers were synthesized for the determination of PRO331:

forward PCR primer: 5'-GCCTTTGACAACCTTCAGTCACTAGTGG-3' (SEQ ID NO:303)

reverse PCR primer 5'-CCCCATGTGTCCATGACTGTTCCC-3' (SEQ ID NO:304)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO331 which had the following nucleotide sequence

hybridization probe

5'-TACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTTAGAGCGG-3'

(SEQ ID NO:305)

Forward and reverse PCR primers were synthesized for the determination of PRO326:

forward PCR primer 5'-ACTCCAAGGAAATCGGATCCGTTC-3' (SEQ ID NO:306)

reverse PCR primer 5'-TTAGCAGCTGAGGATGGGCACAAC-3' (SEQ ID NO:307)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO331 which had the following nucleotide sequence

hybridization probe

5'-GCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGACAACGC-3'

(SEQ ID NO:308)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO335, PRO331 or PRO326 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (PRO335 and PRO326) and human fetal brain (PRO331).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO335, PRO331 or PRO326 [herein designated as SEQ ID NOS:289, 291 and 293, respectively; see Figures 103A-B, 105 and 107, respectively], and the derived protein sequence for PRO335, PRO331 or PRO326 (see Figures 104, 106 and 108, respectively; SEQ ID NOS:290, 292 and 294, respectively).

The entire nucleotide sequences are shown in Figures 103A-B, 105 and 107, deposited with the ATCC on June 2, 1998, November 7, 1997 and November 21, 1997, respectively.

Analysis of the amino acid sequence of the full-length PRO335, PRO331 or PRO326 polypeptide suggests that portions of it possess significant homology to the LIG-1 protein, thereby indicating that PRO335, PRO331 and

PRO326 may be a novel LIG-1-related protein.

EXAMPLE 44: Isolation of cDNA clones Encoding Human PRO332

Based upon an ECD homology search performed as described in Example 1 above, a consensus DNA sequence designated herein as DNA36688 was assembled. Based on the DNA36688 consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO332.

A pair of PCR primers (forward and reverse) were synthesized:

5'-GCATTGGCCGCGAGACTTTGCC-3' (SEQ ID NO:311)

5'-GCGGCCACGGTCCTTGGAAATG-3' (SEQ ID NO:312)

A probe was also synthesized:

5'-TGGAGGAGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGG-3' (SEQ ID NO:313)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO332 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from a human fetal liver library (LIB229).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for DNA40982-1235 and the derived protein sequence for PRO332.

The entire nucleotide sequence of DNA40982-1235 is shown in Figures 109A-B (SEQ ID NO:309). Clone DNA40982-1235 contains a single open reading frame (with an apparent translational initiation site at nucleotide positions 342-344, as indicated in Figures 109A-B). The predicted polypeptide precursor is 642 amino acids long, and has a calculated molecular weight of 72,067 (pI: 6.60). Clone DNA40982-1235 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209433.

Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO332 shows about 30-40% amino acid sequence identity with a series of known proteoglycan sequences, including, for example, fibromodulin and fibromodulin precursor sequences of various species (FMOD_BOVIN, FMOD_CHICK, FMOD RAT, FMOD_MOUSE, FMOD_HUMAN, P_R36773), osteomodulin sequences (AB000114_1, AB007848_1), decorin sequences (CFU83141_1, OCU03394_1, P_R42266, P_R42267, P_R42260, P_R89439), keratan sulfate proteoglycans (BTU48360_1, AF022890_1), corneal proteoglycan (AF022256_1), and bone/cartilage proteoglycans and proteoglycane precursors (PGS1_BOVIN, PGS2_ MOUSE, PGS2_HUMAN).

EXAMPLE 45: Isolation of cDNA clones Encoding Human PRO334

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. Based on the consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO334.

Forward and reverse PCR primers were synthesized for the determination of PRO334:

forward PCR primer 5'-GATGGTTCCTGCTCAAGTGCCCTG-3' (SEQ ID NO:316)

reverse PCR primer 5'-TTGCACTTGTAGGACCCACGTACG-3' (SEQ ID NO:317)

Additionally, a synthetic oligonucleotide hybridization probe was constructed for the determination of PRO334 which had the following nucleotide sequence

hybridization probe

5'-CTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCC-3'

(SEQ ID NO:318)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO334 gene using the probe oligonucleotide and one of the PCR primers.

Human fetal kidney cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO334 [herein designated as DNA41379-1236] (SEQ ID NO:314) and the derived protein sequence for PRO334.

The entire nucleotide sequence of DNA41379-1236 (also referred to as UNQ295) is shown in Figure 109 (SEQ ID NO:314). Clone DNA41379-1236 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 203-205 and ending at the stop codon at nucleotide positions 1730-1732 (Figure 109). The predicted polypeptide precursor is 509 amino acids long (Figure 110). Clone DNA41379-1236 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209488.

Analysis of the amino acid sequence of the full-length PRO334 polypeptide suggests that portions of it possess significant homology to the fibulin and fibrillin proteins, thereby indicating that PRO334 may be a novel member of the EGF protein family.

EXAMPLE 46: Isolation of cDNA Clones Encoding Human PRO346

A consensus DNA sequence was identified using phrap as described in Example 1 above. Specifically, this consensus sequence is herein designated DNA38240. Based on the DNA38240 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length PRO346 coding sequence.

RNA for construction of the cDNA libraries was isolated from human fetal liver. The cDNA libraries used to isolated the cDNA clones were constructed by standard methods using commercially available reagents (e.g., Invitrogen, San Diego, CA; Clontech, etc.) The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA44167-1243 is shown in Figure 111 (SEQ ID NO:319). Clone DNA44167-1243 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 64-66 (Fig. 113; SEQ ID NO:319). The predicted polypeptide

precursor is 450 amino acids long. Clone DNA44167-1243 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209434 (designation DNA44167-1243).

Based on a BLAST, BLAST-2 and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, PRO346 shows amino acid sequence identity to carcinoembryonic antigen (28%).

The oligonucleotide sequences used in the above procedure were the following:

OLI2691 (38240.f1)

5'-GATCCTGTCACAAAGCCAGTGGTGC-3' (SEQ ID NO:321)

OLI2693 (38240.r1)

5'-CACTGACAGGGTTCCTCACCCAGG-3' (SEQ ID NO:322)

OLI2692 (38240.p1)

5'-CTCCCTCTGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATG-3' (SEQ ID NO:323)

EXAMPLE 47: Isolation of cDNA Clones Encoding Human PRO268

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35698. Based on the DNA35698 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO268.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-TGAGGTGGGCAAGCGGCGAAATG-3' (SEQ ID NO:326)

forward PCR primer 2 5'-TATGTGGATCAGGACGTGCC-3' (SEQ ID NO:327)

forward PCR primer 3 5'-TGCAGGGTTCAGTCTAGATTG-3' (SEQ ID NO:328)

reverse PCR primer 5'-TTGAAGGACAAAGGCAATCTGCCAC-3' (SEQ ID NO:329)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA35698 sequence which had the following nucleotide sequence

hybridization probe

5'-GGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGCTGTTGCTTTGGG-3' (SEQ ID NO:330)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO268 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO268 [herein designated as UNQ235 (DNA39427-1179)] (SEQ ID NO:324) and the derived protein sequence for PRO268.

The entire nucleotide sequence of UNQ235 (DNA39427-1179) is shown in Figure 113 (SEQ ID NO:324). Clone UNQ235 (DNA39427-1179) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 13-15 and ending at the stop codon at nucleotide positions 853-855 (Figure 113). The predicted polypeptide precursor is 280 amino acids long (Figure 114). Clone UNQ235 (DNA39427-1179) has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209395.

Analysis of the amino acid sequence of the full-length PRO268 polypeptide suggests that it possess significant homology to protein disulfide isomerase, thereby indicating that PRO268 may be a novel protein disulfide isomerase.

EXAMPLE 48: Isolation of cDNA Clones Encoding Human PRO330

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA35730. Based on the DNA35730 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO330.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-CCAGGCACAATTTCCAGA-3' (SEQ ID NO:333)

forward PCR primer 2 5'-GGACCCTTCTGTGTGCCAG-3' (SEQ ID NO:334)

reverse PCR primer 1 5'-GGTCTCAAGAACTCCTGTC-3' (SEQ ID NO:335)

reverse PCR primer 2 5'-ACACTCAGCATTGCCTGGTACTTG-3' (SEQ ID NO:336)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus sequence which had the following nucleotide sequence

hybridization probe

5'-GGGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAG-3' (SEQ ID NO:337)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO330 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO330 [herein designated as UNQ290 (DNA40603-1232)] (SEQ ID NO:331) and the derived protein sequence for PRO330.

The entire nucleotide sequence of UNQ290 (DNA40603-1232) is shown in Figure 115 (SEQ ID NO:331). Clone UNQ290 (DNA40603-1232) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 167-169 and ending at the stop codon at nucleotide positions 1766-1768 (Figure 115). The predicted polypeptide precursor is 533 amino acids long (Figure 116). Clone UNQ290 (DNA40603-1232) has been deposited with ATCC and is assigned ATCC deposit no.ATCC 209486 on November 21, 1997.

Analysis of the amino acid sequence of the full-length PRO330 polypeptide suggests that portions of it possess significant homology to the mouse prolyl 4-hydroxylase alpha subunit protein, thereby indicating that PRO330 may be a novel prolyl 4-hydroxylase alpha subunit polypeptide.

EXAMPLE 49: Isolation of cDNA Clones Encoding Human PRO310

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA40553. Based on the DNA40553 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO310.

Forward and reverse PCR primers were synthesized:

forward PCR primer 1 5'-TCCCCAAGCCGTTCTAGACGCGG-3' (SEQ ID NO:342)

forward PCR primer 2 5'-CTGGTTCTTCCTTGCACG-3' (SEQ ID NO:343)

reverse PCR primer 5'-GCCCAAATGCCCTAAGGCGGTATACCCC-3' (SEQ ID NO:344)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus sequence which had the following nucleotide sequence

hybridization probe

5'-GGGTGTGATGCTTGGAAGCATTTTCTGTGCTTTGATCACTATGCTAGGAC-3' (SEQ ID NO:345)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO310 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. DNAsequencing of the clones isolated as described above gave the full-length DNA sequence for PRO310 [herein designated as DNA43046-1225 (SEQ ID NO:340) and the derived protein sequence for PRO310 (SEQ ID NO:341).

The entire nucleotide sequence of DNA43046-1225 is shown in Figure 119 (SEQ ID NO:340). Clone DNA43046-1225 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 81-83 and ending at the stop codon at nucleotide positions 1035-1037 (Figure 119). The predicted polypeptide precursor is 318 amino acids long (Figure 120) and has a calculated molecular weight of approximately 36,382 daltons. Clone DNA43046-1225 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209484.

Analysis of the amino acid sequence of the full-length PRO310 polypeptide suggests that portions of it possess homology to *C. elegans* proteins and to fringe, thereby indicating that PRO310 may be involved in development.

EXAMPLE 50: Isolation of cDNA clones Encoding Human PRO339

An expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and ESTs were identified. An assembly of Incyte clones and a consensus sequence was formed using phrap as described in Example 1 above.

Forward and reverse PCR primers were synthesized based upon the assembly-created consensus sequence:

forward PCR primer 1 5'-GGGATGCAGGTGGTGTCTCATGGGG-3' (SEQ ID NO:346)

forward PCR primer 2 5'-CCCTCATGTACCGGCTCC-3' (SEQ ID NO:347)

forward PCR primer 3 5'-GTGTGACACAGCGTGGGC-3' (SEQ ID NO:43)

forward PCR primer 4 5'-GACCGGCAGGCTTCTGCG-3' (SEQ ID NO:44)

reverse PCR primer 1 5'-CAGCAGCTTCAGCCACCAGGAGTGG-3' (SEQ ID NO:45)

reverse PCR primer 2 5'-CTGAGCCGTGGGCTGCAGTCTCGC-3' (SEQ ID NO:46)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus sequence which had the following nucleotide sequence

hybridization probe

5'-CCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGC-3' (SEQ ID NO:47)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pairs identified above. A positive library was then used to isolate clones encoding the PRO339 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal liver tissue. A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA43466-1225 is shown in Figure 117 (SEQ ID NO:338). Clone DNA43466-1225 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 333-335 and ending at the stop codon found at nucleotide positions 2649-2651 (Figure 117; SEQ ID NO:338). The predicted polypeptide precursor is 772 amino acids long and has a calculated molecular weight of approximately 86,226 daltons. Clone DNA43466-1225 has been deposited with ATCC and is assigned ATCC deposit no. ATCC 209490.

Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence, PRO339 has homology to *C. elegans* proteins and collagen-like polymer sequences as well as to fringe, thereby indicating that PRO339 may be involved in development or tissue growth.

EXAMPLE 51: Isolation of cDNA Clones Encoding Human PRO244

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. Based on this consensus sequence, oligonucleotides were synthesized to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for PRO244.

A pair of PCR primers (forward and reverse) were synthesized:

5'-TTCAGCTTCTGGGATGTAGGG-3' (30923.f1) (SEQ ID NO:378)

5'-TATTCCTACCATTTCACAAATCCG-3' (30923.r1) (SEQ ID NO:379)

A probe was also synthesized:

5'-GGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGG-3' (30923.p1) (SEQ ID NO:380)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO244 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from a human fetal kidney library. DNA sequencing of the clones isolated as described above gave the full-length DNA sequence and the derived protein sequence for PRO244.

The entire nucleotide sequence of PRO244 is shown in Figure 121 (SEQ ID NO:376). Clone DNA35668-1171 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 (Fig. 121). The predicted polypeptide precursor is 219 amino acids long. Clone DNA35668-1171 has been deposited with ATCC (designated as DNA35663-1171) and is assigned ATCC deposit no. ATCC209371. The protein has a cytoplasmic domain (aa 1-20), a transmembrane domain (aa 21-46), and an extracellular domain (aa 47-219), with

a C-lectin domain at aa 55-206.

Based on a BLAST and FastA sequence alignment analysis of the full-length sequence, PRO244 shows notable amino acid sequence identity to hepatic lectin gallus gallus (43%), HIC hp120-binding C-type lectin (42%), macrophage lectin 2 (HUMHML2-1, 41%), and sequence PR32188 (44%).

EXAMPLE 52: Use of PRO Polypeptide-Encoding Nucleic Acid as Hybridization Probes

The following method describes use of a nucleotide sequence encoding a PRO polypeptide as a hybridization probe.

DNA comprising the coding sequence of of a PRO polypeptide of interest as disclosed herein may be employed as a probe or used as a basis from which to prepare probes to screen for homologous DNAs (such as those encoding naturally-occurring variants of the PRO polypeptide) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO polypeptide-encoding nucleic acid-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO polypeptide can then be identified using standard techniques known in the art.

EXAMPLE 53: Expression of PRO Polypeptides in *E. coli*

This example illustrates preparation of an unglycosylated form of a desired PRO polypeptide by recombinant expression in *E. coli*.

The DNA sequence encoding the desired PRO polypeptide is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the specific PRO polypeptide coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO polypeptide can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO187, PRO317, PRO301, PRO224 and PRO238 were successfully expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO187, PRO317, PRO301, PRO224 or PRO238 was initially amplified using selected PCR primers. The primers contained restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences were then ligated into an expression vector, which was used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants were first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 was reached. Cultures were then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g $(NH_4)_2SO_4$, 0.71 g sodium citrate·2H2O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM $MgSO_4$) and grown for approximately 20-30 hours at 30°C with shaking. Samples were removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets were frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) was resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution was stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution was centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant was diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. Depending the clarified extract was loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column was washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein was eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein were pooled and stored at 4°C. Protein concentration was estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins were refolded by diluting sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes were chosen so that the final protein concentration was between 50 to 100 micrograms/ml. The refolding solution was stirred gently at 4°C for 12-36 hours. The refolding reaction was quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution was filtered through a 0.22 micron filter and acetonitrile was added to 2-10% final concentration. The refolded protein was chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance were analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein were pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the

most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO187, PRO317, PRO301, PRO224 and PRO238 proteins, respectively, were pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins were formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

EXAMPLE 54: Expression of PRO Polypeptides in Mammalian Cells

This example illustrates preparation of a glycosylated form of a desired PRO polypeptide by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO polypeptide-encoding DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO polypeptide DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO polypeptide.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μg pRK5-PRO polypeptide DNA is mixed with about 1 μg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500 μl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μCi/ml ^{35}S-cysteine and 200 μCi/ml ^{35}S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO polypeptide may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-PRO polypeptide DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μg/ml bovine insulin and 0.1 μg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO polypeptide can then be concentrated and purified by any selected

method, such as dialysis and/or column chromatography.

In another embodiment, PRO polypeptides can be expressed in CHO cells. The pRK5-PRO polypeptide can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S-methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO polypeptide can then be concentrated and purified by any selected method.

Epitope-tagged PRO polypeptide may also be expressed in host CHO cells. The PRO polypeptide may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO polypeptide insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO polypeptide can then be concentrated and purified by any selected method, such as by Ni^{2+}-chelate affinity chromatography.

PRO211, PRO217, PRO230, PRO219, PRO245, PRO221, PRO258, PRO301, PRO224, PRO222, PRO234, PRO229, PRO223, PRO328 and PRO332 were successfully expressed in CHO cells by both a transient and a stable expression procedure. In addition, PRO232, PRO265, PRO246, PRO228, PRO227, PRO220, PRO266, PRO269, PRO287, PRO214, PRO231, PRO233, PRO238, PRO244, PRO235, PRO236, PRO262, PRO239, PRO257, PRO260, PRO263, PRO270, PRO271, PRO272, PRO294, PRO295, PRO293, PRO247, PRO303 and PRO268 were successfully transiently expressed in CHO cells.

Stable expression in CHO cells was performed using the following procedure. The proteins were expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins were fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs were subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas *et al.*, *Nucl. Acids Res.* 24: 9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Fugene® (Boehringer Mannheim). The cells were grown and described in Lucas *et al.*, supra. Approximately 3 x 10^{-7} cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA were thawed by placement into water bath and mixed by vortexing. The contents were pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant was aspirated and the cells were resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells were then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells were transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, a 250 mL, 500 mL and 2000 mL spinners were seeded with 3×10^5 cells/mL. The cell media was exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in US Patent No. 5,122,469, issued June 16, 1992 was actually used. 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH were determined. On day 1, the spinner was sampled and sparging with filtered air was commenced. On day 2, the spinner was sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion). Throughout the production, pH was adjusted as necessary to keep at around 7.2. After 10 days, or until viability dropped below 70%, the cell culture was harvested by centrifugtion and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media was pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of were purified from the conditioned media as follows. The conditioned medium was pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 μL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity was assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

PRO211, PRO217, PRO230, PRO232, PRO187, PRO265, PRO219, PRO246, PRO228, PRO533, PRO245, PRO221, PRO227, PRO220, PRO258, PRO266, PRO269, PRO287, PRO214, PRO317, PRO301, PRO224, PRO222, PRO234, PRO231, PRO229, PRO233, PRO238, PRO223, PRO235, PRO236, PRO262, PRO239, PRO257, PRO260, PRO263, PRO270, PRO271, PRO272, PRO294, PRO295, PRO293, PRO247, PRO304, PRO302, PRO307, PRO303, PRO343, PRO328, PRO326, PRO331, PRO332, PRO334, PRO346, PRO268, PRO330, PRO310 and PRO339 were also successfully transiently expressed in COS cells.

EXAMPLE 55: Expression of PRO Polypeptides in Yeast

The following method describes recombinant expression of a desired PRO polypeptide in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO polypeptides from the ADH2/GAPDH promoter. DNA encoding a desired PRO polypeptide, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of the PRO polypeptide. For secretion, DNA encoding the PRO polypeptide can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of the PRO polypeptide.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO polypeptide can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing the PRO polypeptide may further be purified using selected column chromatography resins.

EXAMPLE 56: Expression of PRO Polypeptides in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO polypeptides in Baculovirus-infected insect cells.

The desired PRO polypeptide is fused upstream of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3 regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO polypeptide can then be purified, for example, by Ni^{2+}-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert *et al.*, *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+}-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL

of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni^{2+}-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His_{10}-tagged PRO polypeptide are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO polypeptide can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

PRO211, PRO217, PRO230, PRO187, PRO265, PRO246, PRO228, PRO533, PRO245, PRO221, PRO220, PRO258, PRO266, PRO269, PRO287, PRO214, PRO301, PRO224, PRO222, PRO234, PRO231, PRO229, PRO235, PRO239, PRO257, PRO272, PRO294, PRO295, PRO328, PRO326, PRO331, PRO334, PRO346 and PRO310 were successfully expressed in baculovirus infected Sf9 or high5 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations. The proteins were expressed as an IgG construct (immunoadhesin), in which the protein extracellular region was fused to an IgG1 constant region sequence containing the hinge, CH2 and CH3 domains and/or in poly-His tagged forms.

Following PCR amplification, the respective coding sequences were subcloned into a baculovirus expression vector (pb.PH.IgG for IgG fusions and pb.PH.His.c for poly-His tagged proteins), and the vector and Baculogold® baculovirus DNA (Pharmingen) were co-transfected into 105 *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711), using Lipofectin (Gibco BRL). pb.PH.IgG and pb.PH.His are modifications of the commercially available baculovirus expression vector pVL1393 (Pharmingen), with modified polylinker regions to include the His or Fc tag sequences. The cells were grown in Hink's TNM-FH medium supplemented with 10% FBS (Hyclone). Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells in Hink's TNM-FH medium supplemented with 10% FBS at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days at 28°C. The supernatant was harvested and the expression of the constructs in the baculovirus expression vector was determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

The first viral amplification supernatant was used to infect a spinner culture (500 ml) of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were incubated for 3 days at 28°C. The supernatant was harvested and filtered. Batch binding and SDS-PAGE analysis was repeated, as necessary, until expression of the spinner culture was confirmed.

The conditioned medium from the transfected cells (0.5 to 3 L) was harvested by centrifugation to remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein construct were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media were pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After

loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins were purified from the conditioned media as follows. The conditioned media were pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of the proteins was verified by SDS polyacrylamide gel (PEG) electrophoresis and N-terminal amino acid sequencing by Edman degradation.

EXAMPLE 57: Preparation of Antibodies that Bind to PRO Polypeptides

This example illustrates preparation of monoclonal antibodies which can specifically bind to a PRO polypeptide.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO polypeptide, fusion proteins containing the PRO polypeptide, and cells expressing recombinant PRO polypeptide on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO polypeptide immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO polypeptide antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO polypeptide. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against the PRO polypeptide. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against the PRO polypeptide is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO polypeptide monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished

using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternanvely, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 58: Chimeric PRO Polypeptides

PRO polypeptides may be expressed as chimeric proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS™ extension/affinity purification system (Immunex Corp., Seattle Wash.). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego Calif.) between the purification domain and the PRO polypeptide sequence may be useful to facilitate expression of DNA encoding the PRO polypeptide.

EXAMPLE 59: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 60: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in

such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 61: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant

structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 62: Diagnostic Test Using PRO317 Polypeptide-Specific Antibodies

Particular anti-PRO317 polypeptide antibodies are useful for the diagnosis of prepathologic conditions, and chronic or acute diseases such as gynecological diseases or ischemic diseases which are characterized by differences in the amount or distribution of PRO317. PRO317 has been found to be expressed in human kidney and is thus likely to be associated with abnormalities or pathologies which affect this organ. Further, since it is so closely related to EBAF-1, it is likely to affect the endometrium and other genital tissues. Further, due to library sources of certain ESTs, it appears that PRO317 may be involved as well in forming blood vessels and hence to be a modulator of angiogenesis.

Diagnostic tests for PRO317 include methods utilizing the antibody and a label to detect PRO317 in human body fluids, tissues, or extracts of such tissues. The polypeptide and antibodies of the present invention may be used with or without modification. Frequently, the polypeptide and antibodies will be labeled by joining them, either covalently or noncovalently, with a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and have been reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent agents, chemiluminescent agents, magnetic particles, and the like. Patents teaching the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. Also, recombinant immunoglobulins may be produced as shown in U.S. Pat. No. 4,816,567.

A variety of protocols for measuring soluble or membrane-bound PRo317, using either polyclonal or monoclonal antibodies specific for that PRO317, are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), radioreceptor assay (RRA), and fluorescent activated cell sorting (FACS). A two-site monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PRO317 is preferred, but a competitive binding assay may be employed. These assays

are described, among other places, in Maddox *et al.* J Exp. Med., 158:1211 (1983).

EXAMPLE 62: Identification of PRO317 Receptors

Purified PRO317 is useful for characterization and purification of specific cell surface receptors and other binding molecules. Cells which respond to PRO317 by metabolic changes or other specific responses are likely to express a receptor for PRO317. Such receptors include, but are not limited to, receptors associated with and activated by tyrosine and serine/threonine kinases. See Kolodziejczyk and Hall, *supra*, for a review on known receptors for the TGF- superfamily. Candidate receptors for this superfamily fall into two primary groups, termed type I and type II receptors. Both types are serine/threonine kinases. Upon activation by the appropriate ligand, type I and type II receptors physically interact to form hetero-oligomers and subsequently activate intracellular signaling cascades, ultimately regulating gene transcription and expression. In addition, TGF- binds to a third receptor class, type III, a membrane-anchored proteoglycan lacking the kinase activity typical of signal transducing molecules.

PRO317 receptors or other PRO317-binding molecules may be identified by interaction with radiolabeled PRO317. Radioactive labels may be incorporated into PRO317 by various methods known in the art. A preferred embodiment is the labeling of primary amino groups in PRO317 with ^{125}I Bolton-Hunter reagent (Bolton and Hunter, Biochem. J., 133:529 (1973)), which has been used to label other polypeptides without concomitant loss of biological activity (Hebert *et al.*, J. Biol. Chem., 266:18989 (1991); McColl *et al.*, J. Immunol., 150:4550-4555 (1993)). Receptor-bearing cells are incubated with labeled PRO317. The cells are then washed to removed unbound PRO317, and receptor-bound PRO317 is quantified. The data obtained using different concentrations of PRO317 are used to calculate values for the number and affinity of receptors.

Labeled PRO317 is useful as a reagent for purification of its specific receptor. In one embodiment of affinity purification, PRO317 is covalently coupled to a chromatography column. Receptor-bearing cells are extracted, and the extract is passed over the column. The receptor binds to the column by virtue of its biological affinity for PRO317. The receptor is recovered from the column and subjected to N-terminal protein sequencing. This amino acid sequence is then used to design degenerate oligonucleotide probes for cloning the receptor gene.

In an alternative method, mRNA is obtained from receptor-bearing cells and made into a cDNA library. The library is transfected into a population of cells, and those cells expressing the receptor are selected using fluorescently labeled PRO317. The receptor is identified by recovering and sequencing recombinant DNA from highly labeled cells.

In another alternative method, antibodies are raised against the surface of receptor bearing cells, specifically monoclonal antibodies. The monoclonal antibodies are screened to identify those which inhibit the binding of labeled PRO317. These monoclonal antibodies are then used in affinity purification or expression cloning of the receptor.

Soluble receptors or other soluble binding molecules are identified in a similar manner. Labeled PRO317 is incubated with extracts or other appropriate materials derived from the uterus. After incubation, PRO317 complexes larger than the size of purified PRO317 are identified by a sizing technique such as size-exclusion chromatography or density gradient centrifugation and are purified by methods known in the art. The soluble receptors or binding protein(s) are subjected to N-terminal sequencing to obtain information sufficient for database identification, if the soluble protein is known, or for cloning, if the soluble protein is unknown.

EXAMPLE 64: Determination of PRO317-Induced Cellular Response

The biological activity of PRO317 is measured, for example, by binding of an PRO317 of the invention to an PRO317 receptor. A test compound is screened as an antagonist for its ability to block binding of PRO317 to the receptor. A test compound is screened as an agonist of the PRO317 for its ability to bind an PRO317 receptor and influence the same physiological events as PRO317 using, for example, the KIRA-ELISA assay described by Sadick *et al.*, Analytical Biochemistry, 235:207-214 (1996) in which activation of a receptor tyrosine kinase is monitored by immuno-capture of the activated receptor and quantitation of the level of ligand-induced phosphorylation. The assay may be adapted to monitor PRO317-induced receptor activation through the use of an PRO317 receptor-specific antibody to capture the activated receptor. These techniques are also applicable to other PRO polypeptides described herein.

EXAMPLE 65: Use of PRO224 for Screening Compounds

PRO224 is expressed in a cell stripped of membrane proteins and capable of expressing PRO224. Low density lipoproteins having a detectable label are added to the cells and incubated for a sufficient time for endocytosis. The cells are washed. The cells are then analysed for label bound to the membrane and within the cell after cell lysis. Detection of the low density lipoproteins within the cell determines that PRO224 is within the family of low density lipoprotein receptor proteins. Members found within this family are then used for screening compounds which affect these receptors, and particularly the uptake of cholesterol via these receptors.

EXAMPLE 66: Ability of PRO Polypeptides to Inhibit Vascular Endothelial Growth Factor (VEGF) Stimulated Proliferation of Endothelial Cell Growth

The ability of various PRO polypeptides to inhibit VEGF stimulated proliferation of endothelial cells was tested. Specifically, bovine adrenal cortical capillary endothelial (ACE) cells (from primary culture, maximum 12-14 passages) were plated on 96-well microtiter plates (Amersham Life Science) at a density of 500 cells/well per 100 μL in low glucose DMEM, 10% calf serum, 2 mM glutamine, 1x pen/strept and fungizone, supplemented with 3 ng/mL VEGF. Controls were plated the same way but some did not include VEGF. A test sample of the PRO polypeptide of interest was added in a 100 μl volume for a 200 μl final volume. Cells were incubated for 6-7 days at 37°C. The media was aspirated and the cells washed 1x with PBS. An acid phosphatase reaction mixture (100 μL, 0.1M sodium acetate, pH 5.5, 0.1% Triton-100, 10 mM p-nitrophenyl phosphate) was added. After incubation for 2 hours at 37°C, the reaction was stopped by addition of 10 μl 1N NaOH. OD was measured on microtiter plate reader at 405 nm. Controls were no cells, cells alone, cells + FGF (5 ng/mL), cells + VEGF (3 ng/mL), cells + VEGF (3 ng/ml) + TGF-β (1 ng/ml), and cells + VEGF (3ng/mL) + LIF (5 ng/mL). (TGF-β at a 1 ng/ml concentration is known to block 70-90% of VEGF stimulated cell proliferation.)

The results were assessed by calculating the percentage inhibition of VEGF (3 ng/ml) stimulated cells proliferation, determined by measuring acid phosphatase activity at OD405 nm, (1) relative to cells without stimulation, and (2) relative to the reference TGF-β inhibition of VEGF stimulated activity. The results, as shown in Table 2 below, are indicative of the utility of the PRO polypeptides in cancer therapy and specifically in inhibiting tumor angiogenesis. The numerical values (relative inhibition) shown in Table 2 are determined by calculating the

percent inhibition of VEGF stimulated proliferation by the PRO polypeptide relative to cells without stimulation and then dividing that percentage into the percent inhibition obtained by TGF-β at 1 ng/ml which is known to block 70-90% of VEGF stimulated cell proliferation.

Table 2

PRO Name	PRO Concentration	Relative Inhibition
PRO211	0.01%	99.0
PRO211	0.01%	1.09
PRO211	0.1%	0.95
PRO211	0.1%	67.0
PRO211	1.0%	0.27
PRO211	1.0%	20.0
PRO217	0.01%	1.06
PRO217	0.1%	0.84
PRO217	1.0%	0.39
PRO217	2.5 μM	0.2
PRO217	25 nM	0.88
PRO217	250 nM	0.58
PRO187	0.01%	0.91
PRO187	0.1%	0.82
PRO187	1.0%	0.44
PRO219	5.7 μM	0.61
PRO219	57 nM	1.09
PRO219	570 nM	0.97
PRO246	0.01%	1.04
PRO246	0.1%	1.0
PRO246	1.0%	0.49
PRO228	0.01%	0.99
PRO228	0.1%	0.93
PRO228	1.0%	0.57
PRO228	0.01%	0.95
PRO228	0.01%	0.98
PRO228	0.1%	0.77
PRO228	0.1%	0.88
PRO228	1.0%	0.16
PRO228	1.0%	0.48
PRO245	0.01%	0.76
PRO245	0.1%	0.35
PRO245	1.0%	0.11
PRO245	0.48 nM	1.03
PRO245	4.8 nM	0.95
PRO245	48 nM	0.49
PRO221	0.01%	1.03
PRO221	0.01%	1.06
PRO221	0.1%	0.82
PRO221	0.1%	0.93
PRO221	1.0%	0.31
PRO221	1.0%	0.43
PRO258	0.01%	0.98
PRO258	0.01%	1.06
PRO258	0.1%	0.95
PRO258	0.1%	1.02
PRO258	1.0%	0.6
PRO258	1.0%	0.69

Table 2 cont'

PRO Name	PRO Concentration	Relative Inhibition
PRO301	7.0 μM	1.02
PRO301	70 μM	0.88
PRO301	700 μM	0.44
PRO301	0.01%	0.92
PRO301	0.1%	0.85
PRO301	1.0%	0.68
PRO224	0.01%	101.0
PRO224	0.1%	65.0
PRO224	1.0%	23.0
PRO272	0.01%	0.95
PRO272	0.1%	0.57
PRO272	1.0%	0.18
PRO328	0.01%	0.98
PRO328	0.1%	0.96
PRO328	1.0%	0.6
PRO331	0.01%	0.88
PRO331	0.1%	0.82
PRO331	1.0%	0.56

EXAMPLE 67: Retinal Neuron Survival

This example demonstrates that PRO220 polypeptides have efficacy in enhancing the survival of retinal neuron cells.

Sprague Dawley rat pups at postnatal day 7 (mixed population: glia and retinal neuronal types) are killed by decapitation following CO_2 anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca^{2+}, Mg^{2+}-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO_2. After 2-3 days in culture, cells are stained with calcein AM then fixed using 4% paraformaldehyde and stained with DAPI for determination of total cell count. The total cells (fluorescent) are quantified at 20X objective magnification using CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The effect of various concentration of PRO220 polypeptides are reported in Table 3 below where percent survival is calculated by dividing the total number of calcein AM positive cells at 2-3 days in culture by the total number of DAPI-labeled cells at 2-3 days in culture. Anything above 30% survival is considered positive.

Table 3

PRO Name	PRO Concentration	Percent Survival
PRO220	0.01%	2.4%
PRO220	0.01%	4.1%
PRO220	0.1%	3.0%
PRO220	0.1%	3.1%
PRO220	1.0%	72.4%
PRO220	1.0%	42.1%

EXAMPLE 68: Rod Photoreceptor Survival

This example demonstrates that PRO220 polypeptides have efficacy in enhancing the survival of rod photoreceptor cells.

Sprague Dawley rat pups at 7 day postnatal (mixed population: glia and retinal neuronal cell types) are killed by decapitation following CO_2 anesthesis and the eyes are removed under sterile conditions. The neural retina is dissected away form the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca^{2+}, Mg^{2+}-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO2. After 2-3 days in culture, cells are fixed using 4% paraformaldehyde, and then stained using CellTracker Green CMFDA. Rho 4D2 (ascites or IgG 1:100), a monoclonal antibody directed towards the visual pigment rhodopsin is used to detect rod photoreceptor cells by indirect immunofluorescence. The results are reported as % survival: total number of calcein/CellTracker - rhodopsin positive cells at 2-3 days.in culture, divided by the total number of rhodopsin positive cells at time 2-3 days in culture. The total cells (fluorescent) are quantified at 20x objective magnification using a CCD camera and NIH image sofrware for MacIntosh. Fields in the well are chosen at random.

The effect of various concentration of PRO220 polypeptides are reported in Table 4 below. Anything above 10% survival is considered positive..

Table 4

PRO Name	PRO Concentration	Percent Survival
PRO220	0.01%	0.0%
PRO220	0.1%	0.0%
PRO220	2.0%	0.0%
PRO220	10%	0.0%
PRO220	20%	66.9%
PRO220	1.0%	56.9%

EXAMPLE 69: Induction of Endothelial Cell Apoptosis

The ability of PRO228 polypeptides to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems), using a 96-well format, in 0% serum media supplemented with 100 ng/ml VEGF. (As HUVEC cells are easily dislodged from the plating surface, all pipetting in the wells must be done as gently as practicable.)

The media was aspired and the cells washed once with PBS. 5 ml of 1 x trypsin was added to the cells in a T-175 flask, and the cells were allowed to stand until they were released from the plate (about 5-10 minutes). Trypsinization was stopped by adding 5 ml of growth media. The cells were spun at 1000 rpm for 5 minutes at 4°C. The media was aspirated and the cells were resuspended in 10 ml of 10% serum complemented medium (Cell Systems), 1 x penn/strep.

The cells were plated on 96-well microtiter plates (Amersham Life Science, cytostar-T scintillating microplate, RPNQ160, sterile, tissue-culture treated, individually wrapped), in 10% serum (CSG-medium, Cell

Systems), at a density of 2 x 10^4 cells per well in a total volume of 100 µl. The PRO228 polypeptide was added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only as a negative control. As a positive control 1:3 serial dilutions of 50 µl of a 3x stock of staurosporine were used. The ability of the PRO228 polypeptide to induce apoptosis was determined using Annexin V, a member of the calcium and phospholipid binding proteins, to detect apoptosis.

0.2 ml Annexin V - Biotin stock solution (100 µg/ml) were diluted in 4.6 ml 2 x Ca^{2+} binding buffer and 2.5% BSA (1:25 dilution). 50 µls of the diluted Annexin V - Biotin solution were added to each well (except controls) to a final concentration of 1.0 µg/ml. The samples were incubated for 10-15 minutes with Annexin-Biotin prior to direct addition of ^{35}S-Streptavidin. ^{35}S-Streptavidin was diluted in 2x Ca^{2+} binding buffer, 2.5% BSA and was added to all wells at a final concentration of 3 x 10^4 cpm/well. The plates were then sealed, centrifuged at 1000 rpm for 15 minutes and placed on orbital shaker for 2 hours. The analysis was performed on 1450 Microbeta Trilux (Wallac). The results are shown in Table 5 below where percent above background represents the percentage amount of counts per minute above the negative controls. Percents greater than or equal to 30% above background are considered positive.

Table 5

PRO Name	PRO Concentration	Percent Above Background
PRO228	0.11%	0.7%
PRO228	0.11%	47.6%
PRO228	0.33%	92.2%
PRO228	0.33%	123.7%
PRO228	1.0%	51.4%
PRO228	1.0%	95.3%

EXAMPLE 70: PDB12 Cell Inhibition

This example demonstrates that various PRO polypeptides have efficacy in inhibiting protein production by PDB12 pancreatic ductal cells.

PDB12 pancreatic ductal cells are plated on fibronectin coated 96 well plates at 1.5x10^3 cells per well in 100 µL/180 µL of growth media. 100 µL of growth media with the PRO polypeptide test sample or negative control lacking the PRO polypeptide is then added to well, for a final volume of 200 µL. Controls contain growth medium containing a protein shown to be inactive in this assay. Cells are incubated for 4 days at 37°C. 20 µL of Alamar Blue Dye (AB) is then added to each well and the flourescent reading is measured at 4 hours post addition of AB, on a microtiter plate reader at 530 nm excitation and 590 nm emission. The standard employed is cells without Bovine Pituitary Extract (BPE) and with various concentrations of BPE. Buffer or CM controls from unknowns are run 2 times on each 96 well plate.

The results from these assays are shown in Table 6 below wherein percent decrease in protein production is calculated by comparing the Alamar Blue Dye calculated protein concentration produced by the PRO polypeptide-treated cells with the Alamar Blue Dye calculated protein concentration produced by the negative control cells. A percent decrease in protein production of greater than or equal to 25% as compared to the negative control cells is considered positive.

Table 6

PRO Name	PRO Concentration	Percent Decrease in Protein Production
PRO211	0.1%	0.0%
PRO211	0.01%	0.6%
PRO211	1.0%	59.7%
PRO287	2.0%	22.3%
PRO287	10%	18.2%
PRO287	50%	67.5%
PRO287	2.0%	45.53%
PRO287	10%	57.3%
PRO287	50%	52.24%
PRO301	2.0%	0.0%
PRO301	10%	59.8%
PRO301	50%	65.6%
PRO293	2.0%	0.0%
PRO293	10%	40.4%
PRO293	50%	56.7%

EXAMPLE 71: Stimulation of Adult Heart Hypertrophy

This assay is designed to measure the ability of various PRO polypeptides to stimulate hypertrophy of adult heart.

Ventricular myocytes freshly isolated from adult (250g) Sprague Dawley rats are plated at 2000 cell/well in 180 μl volume. Cells are isolated and plated on day 1, the PRO polypeptide-containing test samples or growth medium only (negative control) (20 μl volume) is added on day 2 and the cells are then fixed and stained on day 5. After staining, cell size is visualized wherein cells showing no growth enhancement as compared to control cells are given a value of 0.0, cells showing small to moderate growth enhancement as compared to control cells are given a value of 1.0 and cells showing large growth enhancement as compared to control cells are given a value of 2.0. Any degree of growth enhancement as compared to the negative control cells is considered positive for the assay. The results are shown in Table 7 below.

Table 7

PRO Name	PRO Concentration	Growth Enhancement Score
PRO287	20%	1.0
PRO287	20%	1.0
PRO301	20%	1.0
PRO301	20%	1.0
PRO293	20%	1.0
PRO293	20%	1.0
PRO303	20%	1.0
PRO303	20%	1.0

EXAMPLE 72: PDB12 Cell Proliferation

This example demonstrates that various PRO polypeptides have efficacy in inducing proliferation of PDB12 pancreatic ductal cells.

PDB12 pancreatic ductal cells are plated on fibronectin coated 96 well plates at $1.5x10^3$ cells per well in 100 μL/180 μL of growth media. 100 μL of growth media with the PRO polypeptide test sample or negative control

lacking the PRO polypeptide is then added to well, for a final volume of 200 μL. Controls contain growth medium containing a protein shown to be inactive in this assay. Cells are incubated for 4 days at 37°C. 20 μL of Alamar Blue Dye (AB) is then added to each well and the flourescent reading is measured at 4 hours post addition of AB, on a microtiter plate reader at 530 nm excitation and 590 nm emission. The standard employed is cells without Bovine Pituitary Extract (BPE) and with various concentrations of BPE. Buffer or growth medium only controls from unknowns are run 2 times on each 96 well plate.

The results from these assays are shown in Table 8 below wherein percent increase in protein production is calculated by comparing the Alamar Blue Dye calculated protein concentration produced by the PRO polypeptide-treated cells with the Alamar Blue Dye calculated protein concentration produced by the negative control cells. A percent increase in protein production of greater than or equal to 25% as compared to the negative control cells is considered positive.

Table 8

PRO Name	PRO Concentration	Percent Increase in Protein Production
PRO301	2.0%	44.0%
PRO301	10%	67.4%
PRO301	50%	185.8%
PRO303	2.0%	27.9%
PRO303	10%	174.9%
PRO303	50%	193.1%

EXAMPLE 73: Enhancement of Heart Neonatal Hypertrophy Induced by PRO224

This assay is designed to measure the ability of PRO224 polypeptides to stimulate hypertrophy of neonatal heart.

Cardiac myocytes from 1-day old Harlan Sprague Dawley rats were obtained. Cells (180 μl at 7.5 x 10^4/ml, serum <0.1%, freshly isolated) are added on day 1 to 96-well plates previously coated with DMEM/F12 + 4% FCS. Test samples containing the test PRO224 polypeptide or growth medium only (negative control) (20 μl/well) are added directly to the wells on day 1. PGF (20 μl/well) is then added on day 2 at final concentration of 10^{-6} M. The cells are then stained on day 4 and visually scored on day 5, wherein cells showing no increase in size as compared to negative controls are scored 0.0, cells showing a small to moderate increase in size as compared to negative controls are scored 1.0 and cells showing a large increase in size as compared to negative controls are scored 2.0. The results are shown in Table 9 below.

Table 9

PRO Name	PRO Concentration	Growth Enhancement Score
PRO224	0.01%	0.0
PRO224	0.1%	0.0
PRO224	1.0%	1.0

EXAMPLE 74: *In situ* Hybridization

In situ hybridization is a powerful and versatile technique for the detection and localization of nucleic acid sequences within cell or tissue preparations. It may be useful, for example, to identify sites of gene expression,

analyze the tissue distribution of transcription, identify and localize viral infection, follow changes in specific mRNA synthesis and aid in chromosome mapping.

In situ hybridization was performed following an optimized version of the protocol by Lu and Gillett, Cell Vision 1:169-176 (1994), using PCR-generated ^{33}P-labeled riboprobes. Briefly, formalin-fixed, paraffin-embedded human tissues were sectioned, deparaffinized, deproteinated in proteinase K (20 g/ml) for 15 minutes at 37°C, and further processed for *in situ* hybridization as described by Lu and Gillett, *supra*. A [^{33}-P] UTP-labeled antisense riboprobe was generated from a PCR product and hybridized at 55°C overnight. The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

^{33}P-Riboprobe synthesis

6.0 μl (125 mCi) of ^{33}P-UTP (Amersham BF 1002, SA < 2000 Ci/mmol) were speed vac dried. To each tube containing dried ^{33}P-UTP, the following ingredients were added:

2.0 μl 5x transcription buffer

1.0 μl DTT (100 mM)

2.0 μl NTP mix (2.5 mM : 10 μ; each of 10 mM GTP, CTP & ATP + 10 μl H_2O)

1.0 μl UTP (50 μM)

1 0 μl Rnasin

1.0 μl DNA template (1μg)

1.0 μl H_2O

1.0 μl RNA polymerase (for PCR products T3 = AS, T7 = S, usually)

The tubes were incubated at 37°C for one hour. 1.0 μl RQ1 DNase were added, followed by incubation at 37°C for 15 minutes. 90 μl TE (10 mM Tris pH 7.6/1mM EDTA pH 8.0) were added, and the mixture was pipetted onto DE81 paper. The remaining solution was loaded in a Microcon-50 ultrafiltration unit, and spun using program 10 (6 minutes). The filtration unit was inverted over a second tube and spun using program 2 (3 minutes). After the final recovery spin, 100 μl TE were added. 1 μl of the final product was pipetted on DE81 paper and counted in 6 ml of Biofluor II.

The probe was run on a TBE/urea gel. 1-3 μl of the probe or 5 μl of RNA Mrk III were added to 3 μl of loading buffer. After heating on a 95°C heat block for three minutes, the gel was immediately placed on ice. The wells of gel were flushed, the sample loaded, and run at 180-250 volts for 45 minutes. The gel was wrapped in saran wrap and exposed to XAR film with an intensifying screen in -70°C freezer one hour to overnight.

^{33}P-Hybridization

A. Pretreatment of frozen sections

The slides were removed from the freezer, placed on aluminium trays and thawed at room temperature for 5 minutes. The trays were placed in 55°C incubator for five minutes to reduce condensation. The slides were fixed for 10 minutes in 4% paraformaldehyde on ice in the fume hood, and washed in 0.5 x SSC for 5 minutes, at room temperature (25 ml 20 x SSC + 975 ml SQ H_2O). After deproteination in 0.5 μg/ml proteinase K for 10 minutes at 37°C (12.5 μl of 10 mg/ml stock in 250 ml prewarmed RNase-free RNAse buffer), the sections were washed in 0.5 x SSC for 10 minutes at room temperature. The sections were dehydrated in 70%, 95%, 100% ethanol, 2 minutes each.

B Pretreatment of paraffin-embedded sections

The slides were deparaffinized, placed in SQ H_2O, and rinsed twice in 2 x SSC at room temperature, for 5 minutes each time. The sections were deproteinated in 20 μg/ml proteinase K (500 μl of 10 mg/ml in 250 ml RNase-free RNase buffer; 37°C, 15 minutes) - human embryo, or 8 x proteinase K (100 μl in 250 ml Rnase buffer, 37°C, 30 minutes) - formalin tissues. Subsequent rinsing in 0.5 x SSC and dehydration were performed as described above.

C. Prehybridization

The slides were laid out in a plastic box lined with Box buffer (4 x SSC, 50% formamide) - saturated filter paper. The tissue was covered with 50 μl of hybridization buffer (3.75g Dextran Sulfate + 6 ml SQ H_2O), vortexed and heated in the microwave for 2 minutes with the cap loosened. After cooling on ice, 18.75 ml formamide, 3.75 ml 20 x SSC and 9 ml SQ H_2O were added, the tissue was vortexed well, and incubated at 42°C for 1-4 hours.

D. Hybridization

1.0 x 10^6 cpm probe and 1.0 μl tRNA (50 mg/ml stock) per slide were heated at 95°C for 3 minutes. The slides were cooled on ice, and 48 μl hybridization buffer were added per slide. After vortexing, 50 μl ^{33}P mix were added to 50 μl prehybridization on slide. The slides were incubated overnight at 55°C.

E. Washes

Washing was done 2 x 10 minutes with 2xSSC, EDTA at room temperature (400 ml 20 x SSC + 16 ml 0.25M EDTA, V_f=4L), followed by RNaseA treatment at 37°C for 30 minutes (500 μl of 10 mg/ml in 250 ml Rnase buffer = 20 μg/ml). The slides were washed 2 x 10 minutes with 2 x SSC, EDTA at room temperature. The stringency wash conditions were as follows: 2 hours at 55°C, 0.1 x SSC, EDTA (20 ml 20 x SSC + 16 ml EDTA, V_f=4L).

F. Oligonucleotides

In situ analysis was performed on a variety of DNA sequences disclosed herein. The oligonucleotides employed for these analyses are as follows.

(1) DNA33094-1131 (PRO217)

p1 5'-GGATTCTAATACGACTCACTATAGGGCTCAGAAAAGCGCAACAGAGAA-3' (SEQ ID NO:348)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGATGTCTTCCATGCCAACCTTC-3' (SEQ ID NO:349)

(2) DNA33223-1136 (PRO230)

p1 5'-GGATTCTAATACGACTCACTATAGGGCGGCGATGTCCACTGGGGCTAC-3' (SEQ ID NO:350)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGACGAGGAAGATGGGCGGATGGT-3' (SEQ ID NO:351)

(3) DNA34435-1140 (PRO232)

p1 5'-GGATTCTAATACGACTCACTATAGGGCACCCACGCGTCCGGCTGCTT-3' (SEQ ID NO:352)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGACGGGGGACACCACGGACCAGA-3' (SEQ ID NO:353)

(4) DNA35639-1172 (PRO246)

p1 5'-GGATTCTAATACGACTCACTATAGGGCTTGCTGCGGTTTTTGTTCCTG-3' (SEQ ID NO:354)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGCTGCCGATCCCACTGGTATT-3' (SEQ ID NO:355)

(5) DNA49435-1219 (PRO533)

p1 5'-GGATTCTAATACGACTCACTATAGGGCGGATCCTGGCCGGCCTCTG-3' (SEQ ID NO:356)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGCCCGGGCATGGTCTCAGTTA-3' (SEQ ID NO:357)

(6) DNA35638-1141 (PRO245)

p1 5'-GGATTCTAATACGACTCACTATAGGGCGGGAAGATGGCGAGGAGGAG-3' (SEQ ID NO:358)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGACCAAGGCCACAAACGGAAATC-3' (SEQ ID NO:359)

(7) DNA33089-1132 (PRO221)

p1 5'-GGATTCTAATACGACTCACTATAGGGCTGTGCTTTCATTCTGCCAGTA-3' (SEQ ID NO:360)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGGGTACAATTAAGGGGTGGAT-3' (SEQ ID NO:361)

(8) DNA35918-1174 (PRO258)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCCGCCTCGCTCCTGCTCCTG-3' (SEQ ID NO:362)

p2 5 -CTATGAAATTAACCCTCACTAAAGGGAGGATTGCCGCGACCCTCACAG-3' (SEQ ID NO:363)

(9) DNA32286-1191 (PRO214)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCCCTCCTGCCTTCCCTGTCC-3' (SEQ ID NO:364)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGTGGTGGCCGCGATTATCTGC-3' (SEQ ID NO:365)

(10) DNA33221-1133 (PRO224)

p1 5'-GGATTCTAATACGACTCACTATAGGGCGCAGCGATGGCAGCGATGAGG-3' (SEQ ID NO:366)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGACAGACGGGGCAGAGGGAGTG-3' (SEQ ID NO:367)

(11) DNA35557-1137 (PRO234)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCAGGAGGCGTGAGGAGAAAC-3' (SEQ ID NO:368)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAAAGACATGTCATCGGGAGTGG-3' (SEQ ID NO:369)

(12) DNA33100-1159 (PRO229)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCGGGTGGAGGTGGAACAGAAA-3' (SEQ ID NO:370)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGACACAGACAGAGCCCCATACGC-3' (SEQ ID NO:371)

(13) DNA34431-1177 (PRO263)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCAGGGAAATCCGGATGTCTC-3' (SEQ ID NO:372)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGAGTAAGGGGATGCCACCGAGTA-3' (SEQ ID NO:373)

(14) DNA38268-1188 (PRO295)

p1 5'-GGATTCTAATACGACTCACTATAGGGCCAGCTACCCGCAGGAGGAGG-3' (SEQ ID NO:374)

p2 5'-CTATGAAATTAACCCTCACTAAAGGGATCCCAGGTGATGAGGTCCAGA-3' (SEQ ID NO:375)

G. Results

In situ analysis was performed on a variety of DNA sequences disclosed herein. The results from these analyses are as follows.

(1) DNA33094-1131 (PRO217)

Highly distinctive expression pattern, that does not indicate an obvious biological function. In the human embryo it was expressed in outer smooth muscle layer of the GI tract, respiratiry cartilage, branching respiratory epithelium, osteoblasts, tendons, gonad, in the optic nerve head and developing dermis. In the adult expression was observed in the epidermal pegs of the chimp tongue, the basal epithelial/myoepithelial cells of the prostate and urinary bladder. Also expressed in the alveolar lining cells of the adult lung, mesenchymal cells juxtaposed to erectile tissue in the penis and the cerebral cortex (probably glial cells). In the kidney, expression was only seen in disease, in cells surrounding thyroidized renal tubules.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, myocardium, aorta, spleen, lymph node, gall bladder, pancreas, lung, skin, eye (inc. retina), prostate, bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

(a) Chimp Tissues: Salivary gland, stomach, thyroid, parathyroid, skin, thymus, ovary, lymph node.

(b) Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum, penis.

(2) DNA33223-1136 (PRO230)

Sections show an intense signal associated with arterial and venous vessels in the fetus. In arteries the signal appeared to be confined to smooth-muscle/pericytic cells. The signal is also seen in capillary vessels and in glomeruli. It is not clear whether or not endothelial cells are expressing this mRNA. Expression is also observed in epithelial cells in the fetal lens. Strong expression was also seen in cells within placental trophoblastic villi, these cells lie between the trophoblast and the fibroblast-like cells that express HGF - uncertain histogenesis. In the adult, there was no evidence of expression and the wall of the aorta and most vessels appear to be negative. However, expression was seen over vascular channels in the normal prostate and in the epithelium lining the gallbladder. Insurers expression was seen in the vessels of the soft-tissue sarcoma and a renal cell carcinoma. In summary, this is a molecule that shows relatively specific vascular expression in the fetus as well as in some adult organs. Expression was also

observed in the fetal lens and the adult gallbladder.

In a secondary screen, vascular expression was observed, similar to that observed above, seen in fetal blocks. Expression is on vascular smooth muscle, rather than endothelium. Expression also seen in smooth muscle of the developing oesophagus, so as reported previously, this molecule is not vascular specific. Expression was examined in 4 lung and 4 breast carcinomas. Substantial expression was seen in vascular smooth muscle of at least 3/4 lung cancers and 2/4 breast cancers. In addition, in one breast carcinoma, expression was observed in peritumoral stromal cells of uncertain histogenesis (possibly myofibroblasts). No endothelial cell expression was observed in this study.

(3) DNA34435-1140 (PRO232)

Strong expression in prostatic epithelium and bladder epithelium, lower level of expression in bronchial epithelium. High background / low level expression seen in a number of sites, including among others, bone, blood, chondrosarcoma, adult heart and fetal liver. It is felt that this level of signal represents background, partly because signal at this level was seen over the blood. All other tissues negative.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus

In a secondary screen, expression was observed in the epithelium of the prostate, the superficial layers of the urethelium of the urinary bladder, the urethelium lining the renal pelvis and the urethelium of the ureter (1 out of 2 experiments). The urethra of a rhesus monkey was negative; it is unclear whether this represents a true lack of expression by the urethra, or if it is the result of a failure of the probe to cross react with rhesus tissue. The findings in the prostate and bladder are similar to those previously described using an isotopic detection technique. Expression of the mRNA for this antigen is NOT prostate epithelial specific. The antigen may serve as a useful marker for urethelial derived tissues. Expression in the superficial, post-mitotic cells, of the urinary tract epithelium also suggest that it is unlikely to represent a specific stem cell marker, as this would be expected to be expressed specifically in basal epithelium.

(4) DNA35639-1172 (PRO246)

Strongly expressed in fetal vascular endothelium, including tissues of the CNS. Lower level of expression in adult vasculature, including the CNS. Not obviously expressed at higher levels in tumor vascular endothelium. Signal also seen over bone matrix and adult spleen, not obviously cell associated, probably related to non-specific background at these sites.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid,

lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus

(5) DNA49435-1219 (PRO533)

Moderate expression over cortical neurones in the fetal brain. Expression over the inner aspect of the fetal retina, possible expression in the developing lens. Expression over fetal skin, cartilage, small intestine, placental villi and umbilical cord. In adult tissues there is an extremely high level of expression over the gallbladder epithelium. Moderate expression over the adult kidney, gastric and colonic epithelia. Low-level expression was observed over many cell types in many tissues, this may be related to stickiness of the probe, these data should therefore be interpreted with a degree of caution.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum.

(6) DNA35638-1141 (PRO245)

Expression observed in the endothelium lining a subset of fetal and placental vessels. Endothelial expression was confined to these tissue blocks. Expression also observed over intermediate trophoblast cells of placenta. All other tissues negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis

(7) DNA33089-1132 (PRO221)

Specific expression over fetal cerebral white and grey matter, as well as over neurones in the spinal cord. Probe appears to cross react with rat. Low level of expression over cerebellar neurones in adult rhesus brain. All other tissues negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis

(8) DNA35918-1174 (PRO258)

Strong expression in the nervous system. In the rhesus monkey brain expression is observed in cortical, hippocampal and cerebellar neurones. Expression over spinal neurones in the fetal spinal cord, the developing brain and the inner aspects of the fetal retina. Expression over developing dorsal root and autonomic ganglia as well as enteric nerves. Expression observed over ganglion cells in the adult prostate. In the rat, there is strong expression over the developing hind brain and spinal cord. Strong expression over interstitial cells in the placental villi. All other tissues were negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, renal cell carcinoma, adrenal, aorta, spleen, lymph node, pancreas, lung, myocardium, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), bladder, prostate, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis.

(9) DNA32286-1191 (PRO214)

Fetal tissue: Low level throughout mesenchyme. Moderate expression in placental stromal cells in membranous tissues and in thyroid. Low level expression in cortical neurones. Adult tissue: all negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined include: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung and skin.

(10) DNA33221-1133 (PRO224)

Expression limited to vascular endothelium in fetal spleen, adult spleen, fetal liver, adult thyroid and adult lymph node (chimp). Additional site of expression is the developing

spinal ganglia. All other tissues negative.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: Salivary gland, stomach, thyroid, parathyroid, skin, thymus, ovary, lymph node.

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum, penis.

(11) DNA35557-1137 (PRO234)

Specific expression over developing motor neurones in ventral aspect of the fetal spinal cord (will develop into ventral horns of spinal cord). All other tissues negative. Possible role in growth, differentiation and/or development of spinal motor neurons.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetominophen induced liver injury and hepatic cirrhosis

(12) DNA33100-1159 (PRO229)

Striking expression in mononuclear phagocytes (macrophages) of fetal and adult spleen, liver, lymph node and adult thymus (in tingible body macrophages). The highest expression is in the spleen. All other tissues negative. Localisation and homology are entirely consistent with a role as a scavenger receptor for cells of the reticuloendothelial system. Expression also observed in placental mononuclear cells.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, myocardium, aorta, spleen, lymph node, gall bladder, pancreas, lung, skin, eye (inc. retina), prostate, bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: Salivary gland, stomach, thyroid, parathyroid, skin, thymus, ovary, lymph node.

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum, penis.

(13) DNA34431-1177 (PRO263)

Widepread expression in human fetal tissues and placenta over mononuclear cells, probably macrophages +/- lymphocytes. The cellular distribution follows a perivascular pattern in many tissues. Strong expression also seen

in epithelial cells of the fetal adrenal cortex. All adult tissues were negative.

Fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb.

Adult tissues examined: Liver, kidney, adrenal, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), bladder, stomach, colon and colonic carcinoma. Acetominophen induced liver injury and hepatic cirrhosis.

A secondary screen evidenced expression over stromal mononuclear cells probably histiocytes.

(14) DNA38268-1188 (PRO295)

High expression over ganglion cells in human fetal spinal ganglia and over large neurones in the anterior horns of the developing spinal cord. In the adult there is expression in the chimp adrenal medulla (neural), neurones of the rhesus monkey brain (hippocampus [+++] and cerebral cortex) and neurones in ganglia in the normal adult human prostate (the only section that contains ganglion cells, ie expression in this cell type is presumed NOT to be confined to the prostate). All other tissues negative.

Human fetal tissues examined (E12-E16 weeks) include: Placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, great vessels, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb.

Adult human tissues examined: Kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure).

Non-human primate tissues examined:

Chimp Tissues: adrenal

Rhesus Monkey Tissues: Cerebral cortex, hippocampus, cerebellum.

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

Material	ATCC Dep. No.	Deposit Date
DNA32292-1131	ATCC 209258	September 16, 1997
DNA33094-1131	ATCC 209256	September 16, 1997
DNA33223-1136	ATCC 209264	September 16, 1997
DNA34435-1140	ATCC 209250	September 16, 1997
DNA27864-1155	ATCC 209375	October 16, 1997
DNA36350-1158	ATCC 209378	October 16, 1997
DNA32290-1164	ATCC 209384	October 16, 1997
DNA35639-1172	ATCC 209396	October 17, 1997
DNA33092-1202	ATCC 209420	October 28, 1997
DNA49435-1219	ATCC 209480	November 21, 1997
DNA35638-1141	ATCC 209265	September 16, 1997
DNA32298-1132	ATCC 209257	September 16, 1997
DNA33089-1132	ATCC 209262	September 16, 1997
DNA33786-1132	ATCC 209253	September 16, 1997
DNA35918-1174	ATCC 209402	October 17, 1997

DNA37150-1178	ATCC 209401	October 17, 1997
DNA38260-1180	ATCC 209397	October 17, 1997
DNA39969-1185	ATCC 209400	October 17, 1997
DNA32286-1191	ATCC 209385	October 16, 1997
DNA33461-1199	ATCC 209367	October 15, 1997
DNA40628-1216	ATCC 209432	November 7, 1997
DNA33221-1133	ATCC 209263	September 16, 1997
DNA33107-1135	ATCC 209251	September 16, 1997
DNA35557-1137	ATCC 209255	September 16, 1997
DNA34434-1139	ATCC 209252	September 16, 1997
DNA33100-1159	ATCC 209373	October 16, 1997
DNA35600-1162	ATCC 209370	October 16, 1997
DNA34436-1238	ATCC 209523	December 10, 1997
DNA33206-1165	ATCC 209372	October 16, 1997
DNA35558-1167	ATCC 209374	October 16, 1997
DNA35599-1168	ATCC 209373	October 16, 1997
DNA36992-1168	ATCC 209382	October 16, 1997
DNA34407-1169	ATCC 209383	October 16, 1997
DNA35841-1173	ATCC 209403	October 17, 1997
DNA33470-1175	ATCC 209398	October 17, 1997
DNA34431-1177	ATCC 209399	October 17, 1997
DNA39510-1181	ATCC 209392	October 17, 1997
DNA39423-1182	ATCC 209387	October 17, 1997
DNA40620-1183	ATCC 209388	October 17, 1997
DNA40604-1187	ATCC 209394	October 17, 1997
DNA38268-1188	ATCC 209421	October 28, 1997
DNA37151-1193	ATCC 209393	October 17, 1997
DNA35673-1201	ATCC 209418	October 28, 1997
DNA40370-1217	ATCC 209485	November 21, 1997
DNA42551-1217	ATCC 209483	November 21, 1997
DNA39520-1217	ATCC 209482	November 21, 1997
DNA41225-1217	ATCC 209491	November 21, 1997
DNA43318-1217	ATCC 209481	November 21, 1997
DNA40587-1231	ATCC 209438	November 7, 1997
DNA41338-1234	ATCC 209927	June 2, 1998
DNA40981-1234	ATCC 209439	November 7, 1997
DNA37140-1234	ATCC 209489	November 21, 1997
DNA40982-1235	ATCC 209433	November 7, 1997
DNA41379-1236	ATCC 209488	November 21, 1997
DNA44167-1243	ATCC 209434	November 7, 1997
DNA39427-1179	ATCC 209395	October 17, 1997
DNA40603-1232	ATCC 209486	November 21, 1997
DNA43466-1225	ATCC 209490	November 21, 1997
DNA43046-1225	ATCC 209484	November 21, 1997
DNA35668-1171	ATCC 209371	October 16, 1997

These deposit were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined

by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% sequence identity to a nucleotide sequence that encodes a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:12), Figure 9 (SEQ ID NO:18), Figure 11 (SEQ ID NO:23), Figure 13 (SEQ ID NO:28), Figure 15 (SEQ ID NO:34), Figure 17 (SEQ ID NO:39), Figure 19 (SEQ ID NO:49), Figure 22 (SEQ ID NO:59), Figure 24 (SEQ ID NO:64), Figure 26 (SEQ ID NO:69), Figure 28 (SEQ ID NO:71), Figure 30 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:91), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:104), Figure 40 (SEQ ID NO:109), Figure 42 (SEQ ID NO:114), Figure 44 (SEQ ID NO:119), Figure 46 (SEQ ID NO:127), Figure 48 (SEQ ID NO:132), Figure 50 (SEQ ID NO:137), Figure 52 (SEQ ID NO:142), Figure 54 (SEQ ID NO:148), Figure 56 (SEQ ID NO:153), Figure 58 (SEQ ID NO:159), Figure 60 (SEQ ID NO:164), Figure 62 (SEQ ID NO:170), Figure 64 (SEQ ID NO:175), Figure 66 (SEQ ID NO:177), Figure 68 (SEQ ID NO:185), Figure 70 (SEQ ID NO:190), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:201), Figure 76 (SEQ ID NO:207), Figure 78 (SEQ ID NO:213), Figure 80 (SEQ ID NO:221), Figure 82 (SEQ ID NO:227), Figure 84 (SEQ ID NO:236), Figure 86 (SEQ ID NO:245), Figure 88 (SEQ ID NO:250), Figure 90 (SEQ ID NO:255), Figure 92 (SEQ ID NO:257), Figure 94 (SEQ ID NO:259), Figure 96 (SEQ ID NO:261), Figure 98 (SEQ ID NO:263), Figure 100 (SEQ ID NO:285), Figure 102 (SEQ ID NO:290), Figure 104 (SEQ ID NO:292), Figure 106 (SEQ ID NO:294), Figure 108 (SEQ ID NO:310), Figure 110 (SEQ ID NO:315), Figure 112 (SEQ ID NO:320), Figure 114 (SEQ ID NO:325), Figure 116 (SEQ ID NO:332), Figure 118 (SEQ ID NO:339), Figure 120 (SEQ ID NO:341) and Figure 122 (SEQ ID NO:377).

2. The nucleic acid of Claim 1, wherein said nucleotide sequence comprises a nucleotide sequence selected from the group consisting of the sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:11), Figure 8 (SEQ ID NO:17), Figure 10 (SEQ ID NO:22), Figure 12 (SEQ ID NO:27), Figure 14 (SEQ ID NO:33), Figure 16 (SEQ ID NO:38), Figure 18 (SEQ ID NO:48), Figure 21 (SEQ ID NO:58), Figure 23 (SEQ ID NO:63), Figure 25 (SEQ ID NO:68), Figure 27 (SEQ ID NO:70), Figure 29 (SEQ ID NO:72), Figure 31 (SEQ ID NO:83), Figure 33 (SEQ ID NO:90), Figure 35 (SEQ ID NO:95), Figure 37 (SEQ ID NO:103), Figure 39 (SEQ ID NO:108), Figure 41 (SEQ ID NO:113), Figure 43 (SEQ ID NO:118), Figure 45 (SEQ ID NO:126), Figure 47 (SEQ ID NO:131), Figure 49 (SEQ ID NO:136), Figure 51 (SEQ ID NO:141), Figure 53 (SEQ ID NO:147), Figure 55 (SEQ ID NO:152), Figure 57 (SEQ ID NO:158), Figure 59 (SEQ ID NO:163), Figure 61 (SEQ ID NO:169), Figure 63 (SEQ ID NO:174), Figure 65 (SEQ ID NO:176), Figure 67 (SEQ ID NO:184), Figure 69 (SEQ ID NO:189), Figure 71 (SEQ ID NO:194), Figure 73 (SEQ ID NO:200), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:212), Figure 79 (SEQ ID NO:220), Figure 81 (SEQ ID NO:226), Figure 83 (SEQ ID NO:235), Figure 85 (SEQ ID NO:244), Figure 87 (SEQ ID NO:249), Figure 89 (SEQ ID NO:254), Figure 91 (SEQ ID NO:256), Figure 93 (SEQ ID NO:258), Figure 95 (SEQ ID NO:260), Figure 97 (SEQ ID NO:262), Figure 99 (SEQ ID NO:284), Figure 101 (SEQ ID NO:289), Figure 103 (SEQ ID NO:291), Figures 105A-B (SEQ ID NO:293), Figure 107 (SEQ ID NO:309), Figure 109 (SEQ ID NO:314), Figure 111 (SEQ ID NO:319), Figure 113 (SEQ ID NO:324), Figure 115 (SEQ ID NO:331), Figure 117 (SEQ ID NO:338), Figure 119 (SEQ ID NO:340) and Figure 121 (SEQ ID NO:376), or the complement thereof.

3. The nucleic acid of Claim 1, wherein said nucleotide sequence comprises a nucleotide sequence selected from the group consisting of the full-length coding sequence of the sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:11), Figure 8 (SEQ ID NO:17), Figure 10 (SEQ ID NO:22), Figure 12 (SEQ ID NO:27), Figure 14 (SEQ ID NO:33), Figure 16 (SEQ ID NO:38), Figure 18 (SEQ ID NO:48), Figure 21 (SEQ ID NO:58), Figure 23 (SEQ ID NO:63), Figure 25 (SEQ ID NO:68), Figure 27 (SEQ ID NO:70), Figure 29 (SEQ ID NO:72), Figure 31 (SEQ ID NO:83), Figure 33 (SEQ ID NO:90), Figure 35 (SEQ ID NO:95), Figure 37 (SEQ ID NO:103), Figure 39 (SEQ ID NO:108), Figure 41 (SEQ ID NO:113), Figure 43 (SEQ ID NO:118), Figure 45 (SEQ ID NO:126), Figure 47 (SEQ ID NO:131), Figure 49 (SEQ ID NO:136), Figure 51 (SEQ ID NO:141), Figure 53 (SEQ ID NO:147), Figure 55 (SEQ ID NO:152), Figure 57 (SEQ ID NO:158), Figure 59 (SEQ ID NO:163), Figure 61 (SEQ ID NO:169), Figure 63 (SEQ ID NO:174), Figure 65 (SEQ ID NO:176), Figure 67 (SEQ ID NO:184), Figure 69 (SEQ ID NO:189), Figure 71 (SEQ ID NO:194), Figure 73 (SEQ ID NO:200), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:212), Figure 79 (SEQ ID NO:220), Figure 81 (SEQ ID NO:226), Figure 83 (SEQ ID NO:235), Figure 85 (SEQ ID NO:244), Figure 87 (SEQ ID NO:249), Figure 89 (SEQ ID NO:254), Figure 91 (SEQ ID NO:256), Figure 93 (SEQ ID NO:258), Figure 95 (SEQ ID NO:260), Figure 97 (SEQ ID NO:262), Figure 99 (SEQ ID NO:284), Figure 101 (SEQ ID NO:289), Figure 103 (SEQ ID NO:291), Figures 105A-B (SEQ ID NO:293), Figure 107 (SEQ ID NO:309), Figure 109 (SEQ ID NO:314), Figure 111 (SEQ ID NO:319), Figure 113 (SEQ ID NO:324), Figure 115 (SEQ ID NO:331), Figure 117 (SEQ ID NO:338), Figure 119 (SEQ ID NO:340) and Figure 121 (SEQ ID NO:376), or the complement thereof.

4. Isolated nucleic acid which comprises the full-length coding sequence of the DNA deposited under accession number ATCC 209258, ATCC 209256, ATCC 209264, ATCC 209250, ATCC 209375, ATCC 209378, ATCC 209384, ATCC 209396, ATCC 209420, ATCC 209480, ATCC 209265, ATCC 209257, ATCC 209262, ATCC 209253, ATCC 209402, ATCC 209401, ATCC 209397, ATCC 209400, ATCC 209385, ATCC 209367, ATCC 209432, ATCC 209263, ATCC 209251, ATCC 209255, ATCC 209252, ATCC 209373, ATCC 209370, ATCC 209523, ATCC 209372, ATCC 209374, ATCC 209373, ATCC 209382, ATCC 209383, ATCC 209403, ATCC 209398, ATCC 209399, ATCC 209392, ATCC 209387, ATCC 209388, ATCC 209394, ATCC 209421, ATCC 209393, ATCC 209418, ATCC 209485, ATCC 209483, ATCC 209482, ATCC 209491, ATCC 209481, ATCC 209438, ATCC 209927, ATCC 209439, ATCC 209489, ATCC 209433, ATCC 209488, ATCC 209434, ATCC 209395, ATCC 209486, ATCC 209490, ATCC 209484 or ATCC 209371.

5. A vector comprising the nucleic acid of Claim 1.

6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

7. A host cell comprising the vector of Claim 5.

8. The host cell of Claim 7 wherein said cell is a CHO cell.

9. The host cell of Claim 7 wherein said cell is an *E. coli*.

10. The host cell of Claim 7 wherein said cell is a yeast cell.

11. A process for producing a PRO polypeptides comprising culturing the host cell of Claim 7 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

12. Isolated native sequence PRO polypeptide having at least 80% sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:12), Figure 9 (SEQ ID NO:18), Figure 11 (SEQ ID NO:23), Figure 13 (SEQ ID NO:28), Figure 15 (SEQ ID NO:34), Figure 17 (SEQ ID NO:39), Figure 19 (SEQ ID NO:49), Figure 22 (SEQ ID NO:59), Figure 24 (SEQ ID NO:64), Figure 26 (SEQ ID NO:69), Figure 28 (SEQ ID NO:71), Figure 30 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:91), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:104), Figure 40 (SEQ ID NO:109), Figure 42 (SEQ ID NO:114), Figure 44 (SEQ ID NO:119), Figure 46 (SEQ ID NO:127), Figure 48 (SEQ ID NO:132), Figure 50 (SEQ ID NO:137), Figure 52 (SEQ ID NO:142), Figure 54 (SEQ ID NO:148), Figure 56 (SEQ ID NO:153), Figure 58 (SEQ ID NO:159), Figure 60 (SEQ ID NO:164), Figure 62 (SEQ ID NO:170), Figure 64 (SEQ ID NO:175), Figure 66 (SEQ ID NO:177), Figure 68 (SEQ ID NO:185), Figure 70 (SEQ ID NO:190), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:201), Figure 76 (SEQ ID NO:207), Figure 78 (SEQ ID NO:213), Figure 80 (SEQ ID NO:221), Figure 82 (SEQ ID NO:227), Figure 84 (SEQ ID NO:236), Figure 86 (SEQ ID NO:245), Figure 88 (SEQ ID NO:250), Figure 90 (SEQ ID NO:255), Figure 92 (SEQ ID NO:257), Figure 94 (SEQ ID NO:259), Figure 96 (SEQ ID NO:261), Figure 98 (SEQ ID NO:263), Figure 100 (SEQ ID NO:285), Figure 102 (SEQ ID NO:290), Figure 104 (SEQ ID NO:292), Figure 106 (SEQ ID NO:294), Figure 108 (SEQ ID NO:310), Figure 110 (SEQ ID NO:315), Figure 112 (SEQ ID NO:320), Figure 114 (SEQ ID NO:325), Figure 116 (SEQ ID NO:332), Figure 118 (SEQ ID NO:339), Figure 120 (SEQ ID NO:341) and Figure 122 (SEQ ID NO:377).

13. Isolated PRO polypeptide having at least 80% sequence identity to the amino acid sequence encoded by the nucleotide deposited under accession number ATCC 209258, ATCC 209256, ATCC 209264, ATCC 209250, ATCC 209375, ATCC 209378, ATCC 209384, ATCC 209396, ATCC 209420, ATCC 209480, ATCC 209265, ATCC 209257, ATCC 209262, ATCC 209253, ATCC 209402, ATCC 209401, ATCC 209397, ATCC 209400, ATCC 209385, ATCC 209367, ATCC 209432, ATCC 209263, ATCC 209251, ATCC 209255, ATCC 209252, ATCC 209373, ATCC 209370, ATCC 209523, ATCC 209372, ATCC 209374, ATCC 209373, ATCC 209382, ATCC 209383, ATCC 209403, ATCC 209398, ATCC 209399, ATCC 209392, ATCC 209387, ATCC 209388, ATCC 209394, ATCC 209421, ATCC 209393, ATCC 209418, ATCC 209485, ATCC 209483, ATCC 209482, ATCC 209491, ATCC 209481, ATCC 209438, ATCC 209927, ATCC 209439, ATCC 209489, ATCC 209433, ATCC 209488, ATCC 209434, ATCC 209395, ATCC 209486, ATCC 209490, ATCC 209484 or ATCC 209371.

14. A chimeric molecule comprising a polypeptide according to Claim 12 fused to a heterologous amino acid sequence.

15. The chimeric molecule of Claim 14 wherein said heterologous amino acid sequence is an epitope tag sequence.

16. The chimeric molecule of Claim 14 wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

17. An antibody which specifically binds to a PRO polypeptide according to Claim 12.

18. The antibody of Claim 17 wherein said antibody is a monoclonal antibody.

19. Isolated nucleic acid having at least 80% sequence identity to a nucleotide sequence encoding a PRO228 polypeptide having amino acid residues 1 to 690 of Figure 19 (SEQ ID NO:49).

20. The nucleic acid of Claim 19, wherein said nucleotide sequence comprises the nucleotide sequence of Figure 18 (SEQ ID NO:48), or its complement.

21. The nucleic acid of Claim 19, wherein said nucleotide sequence comprises nucleotides 24-2093 of Figure 18 (SEQ ID NO:48), or its complement.

22. An isolated nucleic acid comprising the nucleotide sequence of the full-length coding sequence of clone UNQ202 (DNA33092-1202) deposited under accession number ATCC 209420.

23. An isolated nucleic acid encoding an extracellular domain of a PRO228 polypeptide.

24. A vector comprising the nucleic acid of any one of Claim 19 to 23.

25. The vector of Claim 24 operably linked to control sequences recognized by a host cell transformed with the vector.

26. A host cell comprising the vector of Claim 24.

27. The host cell of Claim 25 wherein said cell is a CHO cell.

28. The host cell of Claim 25 wherein said cell is an *E. coli*.

29. The host cell of Claim 25 wherein said cell is a yeast cell.

30. A process for producing a PRO228 polypeptide comprising culturing the host cell of Claim 25 under conditions suitable for expression of said PRO228 polypeptide and recovering said PRO228 polypeptide from the cell culture.

31. Isolated native sequence PRO228 polypeptide comprising amino acid residues 1 to 690 of Figure 19 (SEQ ID NO:49).

32. An isolated extracellular domain of a PRO228 polypeptide.

33. A chimeric molecule comprising a PRO228 polypeptide fused to a heterologous amino acid sequence.

34. The chimeric molecule of Claim 33 wherein said heterologous amino acid sequence is an epitope ...g sequence

35. The chimeric molecule of Claim 33 wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

36. An antibody which specifically binds to a PRO228 polypeptide.

37. The antibody of Claim 36 wherein said antibody is a monoclonal antibody.

38. A method of inducing apoptosis of tumor cells, said method comprising:

contacting said tumor cells with an apoptosis-inducing amount of a PRO228 polypeptide, wherein apoptosis of said tumor cells is induced.

39. The method according to Claim 39, wherein said contacting in *in vivo*.

FIGURE 1

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCG
CCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCC
GCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTT
TAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGG
AAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCTGGAGGGGCTG
TGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGC
CTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACAC
TGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCC
CAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTC
CTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCA
GCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCCTGCAAGACGTGC
TCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGC
CTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGT
TCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGC
ACAGGGGAAGGCCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACA
GTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACT
GCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGAT
GCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTC
CCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGA
AAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGCCTGCTC
TCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGA
CTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGGAGGAAA
AAAAAA

FIGURE 2

Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
Leu

FIGURE 3

CCAGGCCGGGAGGCGACGCGCCCAGCCGTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC
AGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC
AGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCCGCAGGAGGAGA
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC
CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTCAGAAAAGCGCAACAGAG
AATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG
CAGAATACTTCTATGAATTCCTGTCCTTGCGCTCCCTGGATAAAGGCATCATGGCAGATCCA
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT
CCCATGTCTTGGAAAACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT
CTGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCTTCTTTAAAACATGTCAACAA
GCTGAGTGCCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAATGAAAGACGCATCTGCGAGTG
TCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCCACGATGTATGAATG
GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCCACCTGGATTCTATGGAGTGAACTGT
GACAAAGCAAACTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAATG
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCCACAACCCTGTC
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCCAAAGGTTACCAGGGAGAC
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC
TCATACATGCCCTGAGGCCAGCAGGCGCCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC
GTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCATGTGTTGAATGTTCAAATAA
TGTTCATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT
GATATTTACTCTTCCTTTTAAGTTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTTAAAATTTTCAGTG
TGTACTTGGCAGATATTTTCAAAATTACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT
CAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT
TGAAGTTACAGCATTTCAGATTTTATTGTCAGATATTTAGATGTTTGTTACATTTTTAAAAA
TTGCTCTTAATTTTTAAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT
CAGTATTAAAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAAACAATATAATATATTCTA
AACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT
AAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 4

Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly ProPro Gln
Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCAGTGTGACCAAGAACCATGCCTGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGC
AACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCAT
TCGCTACCGCCTGGGCACCATCCGCCCATCTTCCTCGGTCATGAACATGCATGAAATTTATA
CAGTGCTGAACCCAGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAAC
CTGATTCATGAGCCTCTTGACCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGC
TGTGGCATCCGATCGTGTCTCAATCCATTCTCTGGGACACATGACGCCTGTCCTGTCGCCCC
AGAACCTGCTGTCTTGTGACACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGT
GCCTGGTGGTTCCTGCGTCGCCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCG
TGAACGAGACGAGGCTGGCCCTGCGCCCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGG
GCAAGCGCCAGGCCACTGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTC
ACTCCTGTCTACCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGG
CCCTGTCCAAGCCCTCATGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACA
GCCACACGCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTC
AAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGC
GGCCAACTCCTGGGGCCCAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCA
ATGAGTGCGACATCGAGAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATG
GGTCATCACTGAGGCTGCGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGG
CGGAAGAGGCCCCAATGGGGCGGTGACCCCAGCCTCGCCCGACAGAGCCCGGGGCGCAGGCG
GGCGCCAGGGCGCTAATCCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCCTGGGAGCCGCG
GGCAGGCGAGACTGGCGGAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGG
GAAGAGCACAGCTGCAGATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGA
CACCTCAAGTCTCCAGCCCCAATACCCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGAC
AGGGTCTTGCTCCGTTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCC
GACTCCTGGGTTCAAGTGACCCTCCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCA
CCACCACACCTGGCTAATTTTTGTATTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCCAG
GCTGGTTTCGAACTCCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGAT
TGCAGGCATGAGCCACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTT
TCACTGTTTTAAAATAAAACCAAAGTATTGATAAAAAAAAA

FIGURE 6

><ss.DNA33223
><subunit 1 of 1, 467 aa, 1 stop
><MW: 52387, pI: 6.95, NX(S/T): 2
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRAD
DCALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGTYWD
NCNRCTCQENRQWQCDQEPCLVDPDMIKAINQGNYGWQAGNHSAFWGMTLDEGIRYRLGT
IRPSSSVMNMHEIYTVLNPGEVLPTAFEASEKWPNLIHEPLDQGNCAGSWAFSTAAVASD
RVSIHSLGHMTPVLSPQNLLSCDTHQQQGCRGGRLDGAWWFLRRRGVVSDHCYPFSGRER
DEAGPAPPCMMHSRAMGRGKRQATAHCPNSYVNNNDIYQVTPVYRLGSNDKEIMKELMEN
GPVQALMEVHEDFFLYKGGIYSHTPVSLGRPERYRRHGTHSVKITGWGEETLPDGRTLKY
WTAANSWGPAWGERGHFRIVRGVNECDIESFVLGVWGRVGMEDMGHH

FIGURE 7

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTCGTTGTCTCAAATC
CAATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACAC
CCACCAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCG
CCGAGGGNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGG
CCCTGCGCCCCCCTGTATGATGCACAGCCGAGCCATGGGTCGGGGCAAGCGCCAGGCCAC
TGCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTA
CCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCA
AGCCCTCATGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACAC
GCCAGTGAGCCTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCTCCAACCCTCTCTGCTGCTGTTTCCAT
GGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTTCCC
TGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCAGGG
GACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGAGGA
CAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAAGGG
GCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTTAAT
AAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISKGCSLNCV
DDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLPALGLLLWGPGQL

FIGURE 10

ATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGTGCTTACAGCTGCTGATTCTCTGCTG
TCAAACTCAGTACGTGAGGGACCAGGGCGCCATGACCGACCAGCTGAGCAGGCGGCAGATCC
GCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGTGCAGGTCACCGGGCGTCGCATC
TCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCATAGTGGAGACGGACACGTTTGG
CAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACATCTGTATGAACAAGAGGGGCA
AGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTTCACGGAGATCGTGCTGGAG
AACAACTATACGGCCTTCCAGAACGCCCGGCACGAGGGCTGGTTCATGGCCTTCACGCGGCA
GGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGAGGCCCACTTCATCAAGC
GCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGCCGAGAAGCAGAAGCAGTTCGAGTTT
GTGGGCTCCGCCCCCACCCGCCGGACCAAGCGCACACGGCGGCCCCAGCCCCTCACGTAGTC
TGGGAGGCAGGGGGCAGCAGCCCCTGGGCCGCCTCCCCACCCCTTTCCCTTCTTAATCCAAG
GACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCCTGAGGGCCGCGAA
GCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGCTGGCACAGTGCC
CCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTCACCCTGATCTCAGGCCAC
CAGCCTTTGCCGGCCTCCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTCAGCGACTGAAGGC
CTTGCAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCTCGGATCTCCCTCAGTC
TGCCCCCAGCCCCCAAACTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTTGTTTGTTT
GTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAGAGGGTTGTCCACTCCTCACATTCCA
CGACCCAGGCCTGCACCCCACCCCCAACTCCCAGCCCCGGAATAAAACCATTTTCCTGC

FIGURE 11

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln
Leu Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly
Ala Met Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln
Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg
Arg Ile Ser Ala Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu
Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Ile Lys Gly
Ala Glu Ser Glu Lys Tyr Ile Cys Met Asn Lys Arg Gly Lys Leu
Ile Gly Lys Pro Ser Gly Lys Ser Lys Asp Cys Val Phe Thr Glu
Ile Val Leu Glu Asn Asn Tyr Thr Ala Phe Gln Asn Ala Arg His
Glu Gly Trp Phe Met Ala Phe Thr Arg Gln Gly Arg Pro Arg Gln
Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu Ala His Phe Ile Lys
Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn His Ala Glu Lys
Thr Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr Arg Arg Thr
Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGCTGTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAACAAT
ATTCAGACCATTTCACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCTGGA
TGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCCTCA
AATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGACTTG
CAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTTCCAGAATCT
CACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCGAGG
GCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCCCAC
CCTCCTCCCGATCTCCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGATAAA
CCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCAACA
ACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTCACT
GCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTCACAGAATGGCTCAAATA
TATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGGGGA
TGGCCGTCAGGGAATTAAATATGAATCTTTTGTCCTGTCCCACCACGACCCCCGGCCTGCCT
CTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTATTCC
AAACCCTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAAACTTCCCACGATTCCTG
ACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTTCTGAACGGATCCAGCTCTCTATCCAT
TTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCACCGTGATGGCATACAA
ACTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAGTCA
GCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATTTGT
TTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTCAGAGGCCAC
CACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGACGT
CCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTTGTG
CTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTCCCA
GAAGTGGAAATACAACCGGGGCCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGAAGG
ACAACTCCATCCTGGAGATGACAGAAACCAGTTTTCAGATCGTCTCCTTAAATAACGATCAA
CTCCTTAAAGGAGATTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTACAC
AGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGCACT
GCCATACGTGACAGCCAGAGGCCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAACAC
ACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCATTTG
TGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAAGTGCTA
TCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTAAATCTT

FIGURE 13

><1158/ss.DNA36350

><subunit 1 of 1, 660 aa, 1 stop

><MW: 74049, pI: 8.09, NX(S/T): 7

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLG
IPEGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENN
IQTISRAALAQLLKLEELHLDDNSISTVGVEDGAFREAISLKLLFLSKNHLSSVPVGLPV
DLQELRVDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRN
SLSHPPPDLPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLS
NLKQLTARNNPWFCDCSIKWVTEWLKYIPSSLNVRGFMCQGPEQVRGMAVRELNMNLLSC
PTTTPGLPLFTPAPSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPP
ISERIQLSIHFVNDTSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSL
VNLEPRSTYRICLVPLDAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSP
FLLAGLIGGAVIFVLVVLLSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSIL
DMTETSFQIVSLNNDQLLKGDFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

FIGURE 14A

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCG
CCTCCCACGAGCGATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGG
AAGACCCGGGTGGCTGCGCCCCTGCCTCGCTTCCCAGGCGCCGGCGGCTGCAGCCTTGCCCC
TCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATCCTCGGACAG
ATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTCACGTGGGAGGTCCATCTCTAGGGGCAG
ACACGCTCGGACCCACCCGCAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAG
ACCTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAG
GAGTTCATCGTGGACATCTTGCAATTCTTGGACATTGGTCCTGATGTCACCCGAGTGGGCCT
GCTCCAATATGGCAGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCG
AGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGGGCACCATGACTGGGCTGGCC
ATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCCTGAGGGAGAA
TGTGCCACGGGTCATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGG
CTGCTAAGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTC
AACACCTTGAAGTCCATTGGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTT
CAGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGCACGGCCCACATGTGCA
GCACCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTGGCTCATACGTCTGCAGG
TGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGTGTGC
CATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGT
GCTACAGTGGCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCC
TCAGAAAACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTG
CCATGAAGGATTTGCTCTTAACCCAGATGAAAAAACGTGCACAAGGATCAACTACTGTGCAC
TGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCTACTACTGCCGCTGC
CACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCACA
GCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCCTTCGTCTGCCAGTGCT
CAGAAGGCTTCCTCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTG
AGTGACCATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCCTGTCAGTGTCC
TGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTGCAAAATTGGACTCTTGTGCTCTGG
GGGACCACGGTTGTGAACATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTAT
AGACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGG
AGGGATTCCGGCTCGCTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAAATCAACC
CACCATGGCTGCGAACACATTTGTGTTAATAATGGGAATTCCTACATCTGCAAATGCTCAGA
GGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATTGACC
TGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCGTGAAGCAG
TTTGTCACTGGAATTATAGATTCCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCT
CCAGTATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACA
TGAAAAAAGCCGTGGCCCACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTG
AAACACATGTTTGAGAGAAGTTTTACCCAAGGAGAAGGGGCCAGGCCCCTTTCCACAAGGGT
GCCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGACGTCTCCGAGTGGGCCA
GTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAG
GAACTACAAGAGATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGACTTCAG
CACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCG
ATGGAAGACAGGACTCTCCAGCAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCT
GAGCCAGTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGCAGTGCAACACAG
ATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTTCCCATTCAACAAAAC
CTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC
CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAG
AATGGAAGCCCTGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGT
AGTCATTGTATCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTA
AATCAATAATGTTGTGAAGTAAAACAATCAGTACTGAGAAACCTGGTTTGCCACAGAACAAA
GACAAGAAGTATACACTAACTTGTATAAATTTATCTAGGAAAAAAATCCTTCAGAATTCTAA
GATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAATATACTGTGGACA
CAACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTT

FIGURE 14B

GCACAGTCTTACTTCTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTT
ACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTGGAACAA
GTTGGATTTTTTATACAATATTAAAATTCACCACTTCAG

FIGURE 15

><1164/ss.DNA32290
><subunit 1 of 1, 915 aa, 1 stop
><MW: 102233, pI: 6.02, NX(S/T): 1

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVF
IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV
ERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV
AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH
MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGS
FVCQCYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCT
RINYCALNKPGCEHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNT
EDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGK
TCAKLDSCALGDHGCEHSCVSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHIC
VNSDDSYTCECLEGFRLAEDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAE
DGRRCKKCTEGPIDLVFVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYST
QVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPR
AAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFS
TMDEISEKLKKGICEALEDSDGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQ
HRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLEE
MTQRMEALENRLRYR

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC
CCCCTTGATCTGTACCCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 17

><1172/ss.DNA35639

><subunit 1 of 1, 390 aa, 1 stop

><MW: 41176, pI: 9.61, NX(S/T): 5

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK
PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS
SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

FIGURE 18

CGCCACCACTGCGGCCACCGCCA
><MET {trans=1-s, dir=f, res=1}>
ATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTGTTGAATTGTTCCTATACTCAA
AATTGCACCAAGACACCTTGTCTCCCAAATGCAAAATGTGAAATACGCAATGGAATTGAA
GCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCACAATTTGTGAAGATGATAAT
GAATGTGGAAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGCACTAACACAGAAGGA
AGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCAAGACAGGTTTATC
ACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACTGCCATTTAGATAATGTC
TGTATAGCTGCAAATATTAATAAAACTTTAACAAAAATCAGATCCATAAAAGAACCTGTG
GCTTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTTCACCAACAGATATAATT
ACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAACACTATC
TCAGCCAAGGACACCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAATAAT
TTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAACA
CATCTTACAAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTC
CAAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTT
GATTCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAAT
ATATTTCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTTA
TATTATAAGAGTATTGGTCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAA
AATTATGATAATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATG
AGCTCAAACCCACCCACATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGA
AAGGTCACAGATAGGTATAGGAGTCTATGTGCATTTTGGAATTACTCACCTGATACCATG
AATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCA
TGCCGCTGTAATCACCTGACACATTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGT
ATTAAAGATTATAATATTCTTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATT
TGTCTTGCCATATGCATTTTTACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACA
ACAATTCACAAAAATCTTTGCTGTAGCCTATTTCTTGCTGAACTTGTTTTTCTTGTTGGG
ATCAATACAAATACTAATAAGCTCTTCTGTTCAATCATTGCCGGACTGCTACACTACTTC
TTTTTAGCTGCTTTTGCATGGATGTGCATTGAAGGCATACATCTCTATCTCATTGTTGTG
GGTGTCATCTACAACAAGGGATTTTTGCACAAGAATTTTTATATCTTTGGCTATCTAAGC
CCAGCCGTGGTAGTTGGATTTTCGGCAGCACTAGGATACAGATATTATGGCACAACCAAA
GTATGTTGGCTTAGCACCGAAAACAACTTTATTTGGAGTTTTATAGGACCAGCATGCCTA
ATCATTCTTGTTAATCTCTTGGCTTTTGGAGTCATCATATACAAAGTTTTTCGTCACACT
GCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACATAAGGTCTTGTGCAAGAGGAGCC
CTCGCTCTTCTGTTCCTTCTCGGCACCACCTGGATCTTTGGGGTTCTCCATGTTGTGCAC
GCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGCTTTCCAGGGGATGTTCATT
TTTTTATTCCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAATATTACAGATTGTTCAAA
AATGTCCCCTGTTGTTTTGGATGTTTAAGGTAAACATAGAGAATGGTGGATAATTACAAC
TGCACAAAAATAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAATGACTCATCAAAT
TATCCAATTATTAACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCTGTTTATGCTAT
AGGAACTGTAGATAATAAGGTAAAATTATGTATCATATAGATATACTATGTTTTTCTATG
TGAAATAGTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTGGTTTCTCAGGA
GTGATATCACTGCACCCAAGGAAAGATTTTCTTTCTAACACGAGAAGTATATGAATGTCC
TGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTTGCCTTTGAAACTAGTCCCCT
ACCACCTCGGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGCAGAA
TATCAAACAGTGAAAAGGGAATGATAAGATGTATTTTGAATGAACTGTTTTTTCTGTAGA
CTAGCTGAGAAATTGTTGACATAAAATAAAGAATTGAAGAAACACATTTTACCATTTTGT
GAATTGTTCTGAACTTAAATGTCCACTAAAACAACTTAGACTTCTGTTTGCTAAATCTGT
TTCTTTTTCTAATATTCTAAAAAAAAAAAAAAAGGTTTACCTCCACAAATTGAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33092
><subunit 1 of 1, 690 aa, 0 stop
><MW: 77825, pI: 7.96, NX(S/T): 11
MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDN
ECGNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNV
CIAANINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTI
SAKDTLSNSTLTEFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSF
QKTTEFDTNSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFL
YYKSIGPLLSSSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHR
KVTDRYRSLCAFWNYSPDTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIG
IKDYNILTRITQLGIIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVG
INTNTNKLFCSIIAGLLHYFFLAAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLS
PAVVVGFSAALGYRYYGTTKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHT
AGLKPEVSCFENIRSCARGALALLFLLGTTWIFGVLHVVHASVVTAYLFTVSNAFQGMFI
FLFLCVLSRKIQEEYYRLFKNVPCCFGCLR

FIGURE 20

ATAGGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCA
GAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGAC
ACATTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTA
CAAGGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACC
TTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

CTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCGC
TAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTCACCCCGGCTGGGAC
AAGAAGCCGCCGCCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGGG
GTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAGTCCCGATAAGAAATGCTCGGGT
GTCTTGGGCACCTACCCGTGGGGGCCGTAAGGCGCTACTATATAACGCTGCCGGCCCTGAGC
CGCCGAGCCGTCCGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCACGACCATCCCAACCCGG
CATTCACAGCCCCGCAGCGCATCCGGTCGCCGGCCAGCTTCCGCACCCCATCGCCGGAGCTG
CGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGGATCCT
GGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCCCCACG
TGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCCACGGG
CTCTCCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGCCAGAG
CGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGGCGTGC
ACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGTACTCG
GAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGATCCGA
GAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAACAGAG
GCTTTCTTCCACTCTCTCATTTCCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTGAGGAC
CTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCTGGAGACCGACAGCATGGACCC
ATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACTGAGAC
CATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACGTGCTT
CTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAAGTTGT
ACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGATCATAA
CATTGGAAGCCTTGTACTTGGCCCAGCTGTTGCCTGGGCCCCCCATTCTGCTCCCTCGAGGT
TGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAACTCA
CTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTCTCATCACTTCCCCA
GGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTCAGGAACAGGTGATCCACTCTGTAAAAC
AGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGGACCA
TTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAGGCTT
CAGAAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCCCTGA
GGCCAGTTCTGTCATGGATGCTGTCCTGAGAATAACTTGCTGTCCCGGTGTCACCTGCTTCC
ATCTCCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCTCCCA
GGCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGATTTGA
AGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAACCCTT
TCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACATCTC
TTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTGTTTT
GTATATTAAAATGGAGTTTGTTTGT

FIGURE 22

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly
Leu Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala
Gly Pro His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg
His Leu Tyr Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu
Arg Ile Arg Ala Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser
Ala His Ser Leu Leu Glu Ile Lys Ala Val Ala Leu Arg Thr Val
Ala Ile Lys Gly Val His Ser Val Arg Tyr Leu Cys Met Gly Ala
Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser Glu Glu Asp Cys
Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn Val Tyr Arg
Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala Lys Gln
Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His Phe
Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg
Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp
Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg
Ser Pro Ser Phe Glu Lys

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAACT
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

><ss.DNA35638
><subunit 1 of 1, 312 aa, 1 stop
><MW: 34554, pI: 9.39, NX(S/T): 4
MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT
CATGCTGCTATTCCTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTTGTGGTTCTATGGCATTCATCA
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAACTGAGCAACTTACAAGAACTCTATATTAATCACAACT
TGCTTTCTACAATTTCACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACTTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGGATCTAAATAAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAACCCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTCATGGAGCCAGATTCACTGTTTTGCGTGGACC
CACCTGAATTCCAAGGTCAGAATGTTCGGCAAGTGCATTTCAGGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACTCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAAAATAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCCTAA
AAACCACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLG
LLTFPARLPANTQILLLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQL
LSVYLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQ
MINSKWFDALPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLE
NLESISFYDNRLIKVPHVALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMP
ELISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTI
ESLPNLKEISIHSNPIRCDCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFR
DMMEICLPLIAPESFPSNLNVEAGSYVSFHCRATAEPQPEIYWITPSGQKLLPNTLTDK
FYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRD
IQANSVLVSWKASSKILKSSVKWTAFVKTENSHAAQSARIPSDVKVYNLTHLNPSTEYK
ICIDIPTIYQKNRKKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLISCL
SPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKSTSLKVKATVIGLPTNMS

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTCAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAACA

FIGURE 28

><ss.DNA33089
><subunit 1 of 1, 259 aa, 1 stop
><MW: 29275, pI: 6.92, NX(S/T): 2
MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPR
DLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDL
SDNRIQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEH
AGRPFLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLK
SLPSRQKKADEPDDISTVV

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTCAGGCTCGGCCACGGGCTGCCCGCCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCCACGTGCGCCACGCCCGAGTTTGTCCA
CGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCCGATGGCGACCCGCCGCCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCGTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGGCAGGGACCCCCG
GGCGGCCGGGCAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCCTTCCCACCTC
CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAAACTTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

><ss.DNA33786

><subunit 1 of 1, 620 aa, 1 stop

><MW: 69838, pI: 8.64, NX(S/T): 10

MQVSKRMLAGGVRSMPSPLLACWQPILLLVLGSVLSGSATGCPPRCECSAQDRAVLCHRK
CFVAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFN
LRTLGLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLV
YISHRAFSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYR
LKVLEISHWPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPIS
TIEGSMLHELLRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGN
LETLILDSNPLACDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFT
CRRARIRDRKAQQVFVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDG
TLEVRYAQVQDNGTYLCIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGE
ANSTRATVPFPFDIKTLIIATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPR
KSDAGISSADAPRKFNMKMI

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGGATTCAGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
ACATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGAGGCGCCTGCCCACTTCCTGC
GCCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSS
LQWSNPAQQTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCSIFTMPVR
TAKSLVIVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPT
RIQEDPNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAM
IRPDPPHPREGQKLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSG
TYGCTATSNMGSYKAYYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHY
LIRHKGTYLTHEAKGSDDAPDADTAIINAEGGQSGGDDKKEYFI

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCCAAACCCTTTTCTTCTCCTTTCCTGG
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTACCATTTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACTTCTT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTCACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTTCCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCCTTTTGACAGAAAGCCCAGCACGACCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQ
FYHLFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKI
KSFRKQTFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLILNDNLISTLPANVFQYV
PITHLDLRGNRLKTLPYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALI
GRVVCEAPTRLQGKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQ
EDHATPGSAPNGGTKIPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSG
LKMNCNNRNVSSLADLKPKLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIAT
VENNTFKNLLDLRWLYMDSNYLDTLSREKFAGLQNLEYLNVEYNAIQLILPGTFNAMPK
LRILILNNNLLRSLPVDVFAGVSLSKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPW
ECSCTIVPFKQWAERLGSEVLMSDLKCETPVNFFRKDFMLLSNDEICPQLYARISPTLT
SHSKNSTGLAETGTHSNSYLDTSRVSISVLVPGLLLVFVTSAFTVVGMLVFILRNRKRS
KRRDANSSASEINSLQTVCDSSYWHNGPYNADGAHRVYDCGSHSLSD

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCCAGAATAACTCAGG
GCTGCACCGGGCCTGGCAGCGCTCCGCACACATTTCCTGTCGCGGCCTAAGGGAAACTGT
TGGCCGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTCGGGAGCGAGGGCG
GAGGGGAAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCT
CCAGACACAGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGC
GGGGCCTCAGAGA
><MET {trans=1-s, dir=f, res=1}
ATGAGGCCGGCGTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCGGGCCGGGCGGC
GGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTG
CACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCG
CTCAGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGC
CCAGGGCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCGT
TCCCACTGCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCCTCCGACCCC
GGCGGTCTCGAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCG
CGGAGATGCGCGGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATG
CGATGCCACCTGCGCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCT
GCGCCGCGCCCCGGGGCCGCCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGC
GCCGCTCTGGACTTCAGTCCACCTGGGACCGAGGTGAGTGCGCTCTGCCGGGGACAGCTC
CCGATCTCAGTTACTTGCATCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGC
GATGTGTTGTGTCCCTGCCCCGGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCT
AACTGCCTAGACGACTTGGGAGGCTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGG
AAGGACGGCCGCTCTTGTGTGACCAGTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGG
GTGCCCACCAGGCGCCCGCCGGCCACTGCAACCAGCCCCGTGCCGCAGAGAACATGGCCA
ATCAGGGTCGACGAGAAGCTGGGAGAGACACCACTTGTCCCTGAACAAGACAATTCAGTA
ACATCTATTCCTGAGATTCCTCGATGGGGATCACAGAGCACGATGTCTACCCTTCAAATG
TCCCTTCAAGCCGAGTCAAAGGCCACTATCACCCCATCAGGGAGCGTGATTTCCAAGTTT
AATTCTACGACTTCCTCTGCCACTCCTCAGGCTTTCGACTCCTCCTCTGCCGTGGTCTTC
ATATTTGTGAGCACAGCAGTAGTAGTGTTGGTGATCTTGACCATGACAGTACTGGGGCTT
GTCAAGCTCTGCTTTCACGAAAGCCCCTCTTCCCAGCCAAGGAAGGAGTCTATGGGCCCG
CCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTCCAGTTCTGCACATTGCACA
AACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAGCAGAGGGTGCCTTGCTG
GCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGACATGGGCACTCCTGT
GAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTACTTGTGTAACTGAC
AATTTCTGCAGAAATCCCCCTTCCTCTAAATTCCCTTTACTCCACTGAGGAGCTAAATCA
GAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGATGGTGATAC
TGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAATTTGGAG
AAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACATTAAA
AAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTCAGGCTAGGAGTATATT
GGTTCGAAATCCCAGGGAAAAAAATAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAPALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGA
LSTVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDP
GGLESDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCP
APRPGAASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSG
DVLCPCPGRYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTG
VPTREPPATATSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQM
SLQAESKATITPSGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGL
VKLCFHESPSSQPRKESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALL
AESPLGSSDA

FIGURE 37

CGGACGCGTGGGATTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTA
AGCGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCG
TATCCCCCGGCTACCTGGGCCGCCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGC
AGCCGAGCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTG
GGTGCGGAGGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTAC
GCTGCC
><MET {trans=1-s, dir=f, res=1}
ATGAGGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTC
TCGCGGCAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAG
TCTGGATTTATTGGCAGTGAAGGTTTTCCTGGAGTGTACCCTCCAAATAGCAAATGTACT
TGGAAAATCACAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTC
GAGAGTGACAACCTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGC
CAGCGCATTGGCCGCTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAAC
AAGATGATGGTGCAGATGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATG
TTCTCCGCTGCTGAACCAAACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGA
CCTTCCGGCTCTTTTAAAACCCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACT
TGTGTGTGGCACATTGTAGCCCCAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTT
GATGTGGAGCGAGATAACTACTGCCGATATGATTATGTGGCTGTGTTTAATGGCGGGGAA
GTCAACGATGCTAGAAGAATTGGAAAGTATTGTGGTGATAGTCCACCTGCGCCAATTGTG
TTTCAGAGAAATGAACTTCTTATTCAGTTTTTATCAGACTTAAGTTTAACTGCAGATGGG
TTTATTGGTCACTACATATTCAGGCCAAAAAAACTGCCTACAACTACAGAACAGCCTGTC
ACCACCACATTCCCTGTAACCACGGGTTTAAAACCCACCGTGGCCTTGTGTCAACAAAAG
TGTAGACGGACGGGGACTCTGGAGGGCAATTATTGTTCAAGTGACTTTGTATTAGCCGGC
ACTGTTATCACAACCATCACTCGCGATGGGAGTTTGCACGCCACAGTCTCGATCATCAAC
ATCTACAAAGAGGGAAATTTGGCGATTCAGCAGGCGGGCAAGAACATGAGTGCCAGGCTG
ACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTCTAAATTACATTATTATGGGC
CAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGCTTTATCATGATGTTCAAG
ACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATGTTAACAGTGAACTGTG
TCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCTCTCAGTAGAAAAA
AAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGGGACTGGTTGACT
CTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTTTGCCTGCTGT
CAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGAAGCTAAAA
GTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGATATTTTA
GAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGTGTTA
TTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTAAA
TCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

FIGURE 38

MRGRNAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCT
WKITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGN
KMMVQMISDANIAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVT
CVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIV
SERNELLIQFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTFPVTTGLKPTVALCQQK
CRRTGTLEGNYCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARL
TVVCKQCPLLRRGLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCCACGGCGCCCGCGGGCTGGGGCGGTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCGGCTTGT
TTTGGCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTCACCACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
Ile Lys Gly Arg

FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGG
CAGCACC
><MET (trans=1-s, dir=f, res=1)
ATGCAGCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCTGGCCAGCCCCGGGGCC
GCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGTG
CCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAG
TACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTCAGCCAG
AGCTTCCGAGAGGTGGCCGGCAGGTTCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTG
TTCGGCATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTC
TTCCAGGAGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGC
GCCCGGGCCCGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACC
TCCCTCATCGACTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTG
ACCGAGGCCGTGAACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAG
GTGTCGGTGCAGAGGGAGCATCTGGGCCCGCTGGCGTCCGGCGCCCACAAGCTGGTCCGC
TTTGCCTCGCAGGGGGCGCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTG
GACCTTGGGGACTATGGAGCTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGC
ACCCGCTGCTGCCGCCAGGAGATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAAC
TGGGTGCTGGAGCCCCCGGGCTTCCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCC
CCGGAGGCCCTGGCCTTCAAGTGGCCGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAG
ACTGACTCGCTGCCCATGATCGTCAGCATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTG
GTCAGCCTGCCCAACATGAGGGTGCAGAAGTGCAGCTGTGCCTCGGATGGTGCGCTCGTG
CCAAGGAGGCTCCAGCCATAGGCGCCTAGTGTAGCCATCGAGGGACTTGACTTGTGTGTG
TTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTGGCGATGACTGAACTGCTGATGGACAAA
TGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTTCCTCTGACAAGTTACCTCACCTAAT
TTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGAGAGCCCTTGCTCAGTTTTCTCTA
TTCTTATTATTCACTGCACTATATTCTAAGCACTTACATGTGGAGATACTGTAACCTGAG
GGCAGAAAGCCCANTGTGTCATTGTTTACTTGTCCTGTCACTGGATCTGGGCTAAAGTCC
TCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGTTGTGCATCCCCAATCCA
GATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCTAAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQ
YVALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRL
FQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDV
TEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTL
DLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQP
PEALAFKWPFLGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALV
PRRLQP

FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTCGCAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCA

FIGURE 44

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCAGGCCCCAGCTCAG
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTCGGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

><ss.DNA33221
><subunit 1 of 1, 282 aa, 1 stop
><MW: 28991, pI: 4.62, NX(S/T): 3
MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQ
CRTSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGT
DKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATT
MGPPVTLESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSA
SLVTATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAACTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCCTAAGAAACTGATTGATTAAAAAATTTCCCAAAGTGTCCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

FIGURE 48

><ss.DNA33107
><subunit 1 of 1, 490 aa, 1 stop
><MW: 53920, pI: 5.41, NX(S/T): 4
MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADP
GIPENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQE
DCRIPQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGC
LRPLASSNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLAL
EAQVCPLPPMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSY
QVYCIKSEQTWPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPR
SSSSDPDFVVVDGVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSG
DTDTGPGESETCDSVSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIH
HAHWVLFLRN

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTCGCCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCATTCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTTCCTTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCA
CAGGTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAA
AGAGCAGGAAAAAAAAA

FIGURE 50

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTTATACAATG

FIGURE 52

><ss.DNA34434
><subunit 1 of 1, 428 aa, 1 stop
><MW: 48886, pI: 6.39, NX(S/T): 0
MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHG
ARSPLKPLPLEEQVEWNPQLLEVPPQTQPDYTVTNLAGGPKPYSPYDSQYHETTLKGGMF
AGQLTKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGL
FQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMG
IDSSDKVDFFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMA
VGPFLHILESNLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLT
MELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVYTLSPEKYHALCSQTQ
VMEVGNEE

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTCACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTCAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

>ss.DNA33100

>subunit 1 of 1, 347 aa, 1 stop

>MW: 38130, pI: 5.40, NX(S/T): 0

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAV
LCRELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDA
GASCENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLG
CGRAVLTQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECED
PFDLRLVGGDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKC
YGPGVGRIWLDNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

FIGURE 56

><ss.DNA35600

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33524, pI: 9.55, NX(S/T): 1

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAA
GAKLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGY
VDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSI
QGKMSIPFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSR
YGVMDTTTAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASR
ARKERKSKNS

FIGURE 57

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGG
><MET {trans=1-s, dir=f, res=1}>
ATGAAATTTCTTCTGGACATCCTCCTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTC
CTTCGTGAAGCTTTTTATTCCTAAGAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTA
CAGGAGCTGGGCATGGAATTGGGAGACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAG
CTGGTTCTCTGGGATATAAATAAGCATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACT
GGGTGCCAAGGTTCATACCTTTGTGGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTG
CAAAGAAGGTGAAGGCAGAAATTGGAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTC
TATACATCAGATTTGTTTGCTACACAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGT
ACTTGCACATTTCTGGACTACAAAGGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCC
ATATTGTCACTGTGGCTTCGGCAGCTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGT
TCAAGCAAGTTTGCTGCTGTTGGATTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACA
AATAACTGGAGTCAAAACAACATGTCTGTGTCCTAATTTCGTAAACACTGGCTTCATCAAAA
ATCCAAGTACAAGTTTGGGACCCACTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCAT
GGGATTCTGACTGAGCAGAAGATGATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATT
GGAAAGGATCCTTCCTGAGCGTTTCCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTG
ATGCAGTTATTGGATATAAAATGAAAGCGCAATAAGCACCTAGTTTTCTGAAAACTGATTTA
CCAGGTTTAGGTTGATGTCATCTAATAGTGCCAGAATTTTAATGTTTGAACTTCTGTTTTTT
CTAATTATCCCCATTTCTTCAATATCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCAC
TTGTTCTTTAGCCAAAAGCTGATTACATATGATATAAACAGAGAAATACCTTTAGAGGTGAC
TTTAAGGAAAATGAAGAAAAAGAACCAAAATGACTTTATTAAAATAATTTCCAAGATTATTT
GTGGCTCACCTGAAGGCTTTGCAAAATTTGTACCATAACCGTTTATTTAACATATATTTTTA
TTTTTGATTGCACTTAAATTTTGTATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAG
AAACTTCAAGCTCTCTAAATAAAATGAAGGACTATATCTAGTGGTATTTCACAATGAATATC
ATGAACTCTCAATGGGTAGGTTTCATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCT
CACATTCCAATGCCAAACATTTCTGCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGT
ATAAAAGCATCACTGGGATTTAAGGAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAA
TAAATGGATCACACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

> < subunit 1 of 1, 300 aa, 1 stop

> < MW: 32964, pI: 9.52

><signal peptide>

MKFLLDILLLLPLLIVCSL

><start mature protein>

ESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKLVLWDINKHGLEETAAK

CKGLGAKVHTFVVDCSNREDIYSSAKKVKAEIGDVSILVNNAGVVYTSDLFATQDPQIEK

TFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLA

><putative oxidoreductase active site, by similarity to Y00P_MYCTU and BUDC_KLETE>

YCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVN

RLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTCAGTTTTTCCAGATATTTCCTGAATATAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACTATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAAAGTTTGGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAAGTAAAAAAAAAA

FIGURE 60

><ss.DNA33206
><subunit 1 of 1, 476 aa, 1 stop
><MW: 54164, pI: 5.52, NX(S/T): 4

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
SLVGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGL
FVEHGPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLY
SALIQFFQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYS
DPESIIGGYAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTS
DPSYFQNVTGCSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR
EDTVQSVKPWLTEIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKKVWK
IFKSDSEVAGYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG
TGAACTTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACCACCCGCCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTTTGTG
ACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACTTTAAGAAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

><ss.DNA35558
><subunit 1 of 1, 552 aa, 1 stop
><MW: 61674, pI: 6.95, NX(S/T): 4
MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQP
WPRALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGA
INRVYKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRL
LACGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGT
AVDGKQDYFPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYG
FASGGFVYFLTVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVE
YRLLQAAYLAKPGDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQ
IKERLQSCYQGEGNLELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYT
TSRDRMTSVASYVYNGYSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRF
NYRQLYFLGEQR

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAA
CACGCGATGACCACGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGGACTCCTGCTGCT
GGTCGTCTTGGGCTTCCTGGTGCTCCGCAGGCTGGACTGGAGCACCCTGGTCCCTCTGCGGC
TCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGAACTTCATGCTGGAGGATTCCACC
TTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACTGGAGGGACCG
CCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGC
ATGAGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCCTG
ATGGCCGCAGAGATCGGGCTGTGGGTGATTCTGCGTCCAGGCCCCTACATCTGCAGTGAGAT
GGACCTCGGGGGCTTGCCCAGCTGGCTACTCCAAGACCCTGGCATGAGGCTGAGGACAACTT
ACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACCTGATGTCCAGGGTGGTGCCA
CTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATGGTTCCTA
TAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGG
AACTGCTCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTG
GCCACCATCAACTTGCAGTCAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGT
CCAGGGGACTCAGCCCAAGATGGTGATGGAGTACTGGACGGGGTGGTTTGACTCGTGGGGAG
GCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGTCTGCCATTGTGGACGCC
GGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATGGAGC
CATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAG
AAGCCGGCGATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGC
ATCCCTCTCCCTCCCCCACCTGACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGT
CTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACCTGGGGGAGCCAATCAAGTCTGAAAAGC
CCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCTTCGGGTACATTCTC
TATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGGT
GTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCC
TGATCCAGGGTTACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGG
GAGAATATTGATGACCAGCGCAAAGGCTTAATTGGAAATCTCTATCTGAATGATTCACCCCT
GAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGAGCTTCTTTCAGAGGTTCGGCCTGG
ACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGGGTAGCTTGTCC
ATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATT
CATCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTTACCTCC
CAGGTCCCTGGTTGAGCAGCGGAATCAACCAGGTCATCGTTTTTGAGGAGACGATGGCGGGC
CCTGCATTACAGTTCACGGAAACCCCCCACCTGGGCAGGAACCAGTACATTAAGTGAGCGGT
GGCACCCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTCCTCTTGACCTGAAGCCTGGTG
GCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGGACTGGGGG
CTACAGTCTGCCCCTGTCTCAGCTCAAAACCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCT
GGGCCTGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTCGGGC
TGTCTCTAGGGTGGGAGCAGCTAATCAGATCGCCCAGCCTTTGGCCCTCAGAAAAAGTGCTG
AAACGTGCCCTTGCACCGGACGTCACAGCCCTGCGAGCATCTGCTGGACTCAGGCGTGCTCT
TTGCTGGTTCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCATTTTATCCCCGAAATCCTG
GGTGTGTCACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTTCTTCC
TTCACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGAC
TTCCCCTTTCCCTTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGA
AATCCTCACCCTGCGTCTTCCCAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATG
TGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGAAGGCCCAG
CTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGGACAGA
AGGCCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGG
AGGACAGAAGGCCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATC
CAGGGAGGAGGACAGAAGGCCCAGCTCAGTGGCCCCCGCTCCCCACCCCCCACGCCCGAACA
GCAGGGGCAGAGCAGCCCTCCTTCGAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTTCTGGG
GCCCAGCCCAACACCTGGCTTGGGCTCACTGTCCTGAGTTGCAGTAAAGCTATAACCTTGAA
TCACAA

FIGURE 64

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDS
TFWIFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLE
AFVLMAAEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDH
LMSRVVPLQYKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDG
LSKGIVQGVLATINLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFDSWGGPHNILDS
SEVLKTVSAIVDAGSSINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY
TAKYMKLRDFFGSISGIPLPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPI
NMENLPVNGGNGQSFGYILYETSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAV
PLIQGYTVLRILVENRGRVNYGENIDDQRKGLIGNLYLNDSPLKNFRIYSLDMKKSFFQ
PFGLDKWXSLPETPTLPAFFLGSLSISSTPCDTFLKLEGWEKGVVFINGQNLGRYWNIG
PQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLGRNQYIK

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
GGCAGACACTCGGTCGTTCGTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTCAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCCTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCTCTACGTGCCAAGATTCCTGCTGTTTCCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAA

FIGURE 66

MRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICAEW
EMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEY
GSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTK
IFTLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYMFH
GGTNFGYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLP
PPSPKMMLGPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHT
IFEPTPFWVPNNGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLS
FGSNSSDFKGLLKPPILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFY
SKTFPILGSVGDTFLYLPGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALN
KITLLELEDVPLQPQVQFLDKPILNSTSTLHRTHINSLSADTLSASEPMELSGH

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTCACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAACT
AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
GACTTGTTTAAAATTATGGCATAACAAAATTGTTACTATTCCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAA

FIGURE 68

><ss.DNA34407
><subunit 1 of 1, 501 aa, 1 stop
><MW: 57819, pI: 8.15, NX(S/T): 3
MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFA
FLLHMVDQYDQLYSKRFGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLF
MLSGVPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRD
HLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRHLKILHVKS
NLTKVPSNITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSL
SNLQELDLKSNNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNK
LESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKL
RTLNLGQNCITSLPEKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDT
LPLEVKEALNQDINIPFANGI

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCTTTTCATTGACAAACTGAC
TTTTTTTATTTCTTTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGA
CATTTGTGTTTTACACACATAAGGATCTGTGTTTGGGGTTTCTTCTTCCTCCCCTGACATTG
GCATTGCTTAGTGGTTGTGTGGGGAGGGAGACCACGTGGGCTCAGTGCTTGCTTGCACTTAT
CTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTCATCGCTGGTG
GTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAAATACAC
AACGCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAA
GGTGTGGTGGGCCAAGAACAGCCAGGCCAAAACCATTGCCACGGAGTCTTGTCCTGCCCTGC
AGTGCTGTGAAGGATATAGAATGTGTGCCAGTTTTGATTCCCTGCCACCTTGCTGTTGCGAC
ATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAAAGCAGAGCCCTGAAGACTTCA
ATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAGCTCCCCA
TCAGTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAG
AGCTTCCACTGGGGGCAACCCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGG
AATGCTGATAAACCAGTCACACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCT
GGAACTGACGTTTCCCTGGAGGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTG
TCGGTCCTTAAGGCTGCCCAGCGCCTTGCCAAAATGGAGCTTGTAAGAAGGCTCATGCCATT
GACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAATGCAA
GCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAA
CTCAATCCCAGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAAT
TATCTTTTCCTATGTCCAGCTTGATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCT
TTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGGCAAGTCTGCAGTAAAAACGACTATGTT
CCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACTGACTCAGCAAGAAT
TCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAAACTGTG
GCGGTTACCTGGATACCTTGGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCT
GAGCTGGCTTATTGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTT
CAAAGAGATTTTCCTAGAAATAGACAAACAGTGCAAATTTGATTTTCTTGCCATCTATGATG
GCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGTGGCCGTGTGACTCCCACCTTCGAA
TCGTCATCAAACTCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCTTACCGGGGATT
TTCTGCTTCCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTT
CTGACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAAT
AACTTGCAACTAAAAGACCCAACTTGCAGACCAAAATTATCAAATGTTGTGGAATTTTCTGT
CCCTCTTAATGGATGTGGTACAATCAGAAAGGTAGAAGATCAGTCAATTACTTACACCAATA
TAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACCCGTCAGAAACAACTCCAGATT
ATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACAGAAGATGA
TGTAATACAAAGTCAAAATGCACTGGGCAAATATAACACCAGCATGGCTCTTTTTGAATCCA
ATTCATTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACTCTTTTT
GTTCAAGTTAGTCTGCACACCTCAGATCCAAATTTGGTGGTGTTTCTTGATACCTGTAGAGC
CTCTCCCACCTCTGACTTTGCATCTCCAACCTACGACCTAATCAAGAGTGGATGTAGTCGAG
ATGAAACTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGATTCCAGTTTAATGCCTTT
AAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTTGATATGTGATAGCAG
TGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCAT
ATAAATGGAAAACAGATTCCATCATAGGACCCATTCGTCTGAAAAGGGATCGAAGTGCAAGT
GGCAATTCAGGATTTCAGCATGAAACACATGCGGAAGAAACTCCAAACCAGCCTTTCAACAG
TGTGCATCTGTTTTCCTTCATGGTTCTAGCTCTGAATGTGGTGACTGTAGCGACAATCACAG
TGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTGCAGAACTATTAACTA
ACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGTGG
CTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

FIGURE 70

>ss.DNA35841

>subunit 1 of 1, 607 aa, 1 stop

>MW: 68153, pI: 6.39, NX(S/T): 9

MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTW
TIERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSS
STLTFQIVTDSARIQRTVFVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYC
VWHIQVEKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSS
NSLTVVLSTDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNN
LQLKDPTCRPKLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQ
IIVKCEMGHNSTVEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQ
TLFVQVSLHTSDPNLVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRF
QFNAFKFLRSMSSVYLQCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSIIGPIRL
KRDRSASGNSGFQHETHAEETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYK
YQKLQNY

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC
TGCTGCCGCCGCCGCCGTGCCCTGCCCACAGCGCCACGCGCTTCGACCCCACCTGGGAGTCC
CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAACTGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGACTGTACTATTCCCTTTTTGA
ATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACTGCATGACAATAGACAAACTGTCCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTTCTGTAGTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCCACATCAGGACAGCTGTTCCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAATT
TTTAAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAAACATAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFI
HWGVFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWA
DIFQASGAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRF
GLYYSLFEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQ
YWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCM
TIDKLSWGYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLR
QVGSWLKVNGEAIYETYTWRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHP
KAILGATEVKLLGHGQPLNWISLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTTGTGTCACAGAAGTTTTTATGGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCGATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGAC
CCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTTATTTTTGCTGAGACTAATCTT
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA
GCCCTCCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAAACTT

FIGURE 74

><ss.DNA34431
><subunit 1 of 1, 322 aa, 1 stop
><MW: 35213, pI: 8.71, NX(S/T): 3
MARCFSLVLLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEA
CRLLGLSLAGKDQVETALKASFETCSYGWVGDGFVVISRISPNPKCGKNGVGVLIWKVPV
SRQFAAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPA
PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTAL
LVLALLFFGAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKT
DKNPEESKSPSKTTVRCLEAEV

FIGURE 75

AG

><MET {trans=1-s, dir=f, res=1}>

ATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGG
AAACTGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGAC
TTTGACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAAC
CGCAGATCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCC
AACACAATTCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGC
ATAGTGTTCCTGATGACGTGCAAACCCCCCCTATATATGGGCCCTGAGTATATCAAGTAC
TTCAATGATAAAACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTG
GAGTTCTTTGCCAATTGGTCTAATGACTGCCAATCATTTGCCCCTATCTATGCTGACCTC
TCCCTTAAATACAACTGTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACT
GATGTTAGTACGCGGTACAAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTG
ATCCTGTTCCAAGGTGGCAAGGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGG
GCTGTCTCATGGACCTTCTCTGAGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTA
TACCAGCGGGCCAAGAAACTATCAAAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTG
GCTTCAACCCCCACCACAGTGTCAGATGGGGAAAACAAGAAGGATAAATAAGATCCTCAC
TTTGGCAGTGCTTCCTCTCCTGTCAATTCCAGGCTCTTTCCATAACCACAAGCCTGAGGC
TGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGGCAGCATGCAGCTTC
TGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGCCTGCCATGCTG
TGGCCAACTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGAAATGGTTT
CCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATCAGCTATTCAGACATCTCCATGGTT
TCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTTAG
ACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAA
GGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGC
CTAACTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTATCATTGAAGA
CAATATTGAACAACCCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGAC
TTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCACTAACCCTCTGAC
ATACTCCCCACACCCAGTTGATGGCTTTCCGTAATAAAAAGATTGGGATTTCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCD
FDWREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLC
IVFLMTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADL
SLKYNCTGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGR
AVSWTFSEENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

FIGURE 77

GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCGGGTCACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCCGCCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTACTATTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCCT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCCTCCCCGTTCCCCT
TCCCCTCTCGGTTCCAAAGAATCTGTTTTGTTGTCATTTGTTTCTCCTGTTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 78

><ss.DNA39423
><subunit 1 of 1, 360 aa, 1 stop
><MW: 40894, pI: 6.44, NX(S/T): 0
MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFT
YQGASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVH
LRQDKEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFN
FHEGQQVCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAP
GVRSYGPRHRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLF
AAWKFHGLDRCDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG

><MET {trans=1-s, dir=f, res=1}

ATGATGTGGCGACCATCAGTTCTGCTGCTTCTGTTGCTACTGAGGCACGGGGCCCAGGGG
AAGCCATCCCCAGACGCAGGCCCTCATGGCCAGGGGAGGGTGCACCAGGCGGCCCCCCTG
AGCGACGCTCCCCATGATGACGCCCACGGGAACTTCCAGTACGACCATGAGGCTTTCCTG
GGACGGGAAGTGGCCAAGGAATTCGACCAACTCACCCCAGAGGAAAGCCAGGCCCGTCTG
GGGCGGATCGTGGACCGCATGGACCGCGCGGGGGACGGCGACGGCTGGGTGTCGCTGGCC
GAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCACATACGGGACTCGGTGAGCGCG
GCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGGGTTGGGAGGAGCTGCGCAAC
GCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTCATGACGTGGAGGATGCAGAGACC
TACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGCCGACCAGGATGGGGAC
TCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGGAGTTCCCTCACATG
CGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAAGATGGCTATGTC
CAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGAGGAGCCGGCG
TGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGGATGGGCAC
CTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCCCTGGTG
GAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAAAGCG
GAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGGAC
CTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGG
AGGCAGATGCAGTCCCAGGCATCCTCCTGCCCCTGGGCTCTCAGGGACCCCCTGGGTCGG
CTTCTGTCCCTGTCACACCCCCAACCCCAGGGAGGGGCTGTCATAGTCCCAGAGGATAAG
CAATACCTATTTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTC
AGCTCTAAGAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTG
AAACTCCCCTGGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCC
AGGAGGCAATAAAAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 80

>></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40620
>><subunit 1 of 1, 328 aa, 0 stop
>><MW: 37493, pI: 4.77, NX(S/T): 1
MMWRPSVLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFL
GREVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSA
AWDTYDTDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD
SMATREELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPA
WVQTERQQFRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKA
EILGNWNMFVGSQATNYGEDLTRHHDEL

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCC
GGGCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTC
CCAGCCTGTCTGTCGTCGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTGCACACCG
ATCCTGGGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCC
TGGAGCAGCGGGTCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGT
GCGGGGCTCTGAGGAGGTGACGCGCGGGGCCTCCCGCACCCTGGCCTTGCCCGCATTCTC
CCTCTCTCCCAGGTGTGAGCAGCCTATCAGTCACC
><MET {trans=1-s, dir=f, res=1}
ATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTGTCTGCTGCTGCTGCCGGGG
CCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATGTTTTACCAGAGGCTTGGAC
ATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCCCTCTTGAGGAATTCTCT
GTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCCACAGG
GGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAAAC
TATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCT
TTCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACA
GCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACTGGCAATAAA
GATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGA
TTTAATTTACAGAAGAATTTTGTTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACAGAA
GGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAAA
AACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGT
AATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCT
GGAGTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGAT
GACATCGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCT
GTGGCCAAGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAG
GCTGTCTGTCGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACA
AAATACGTAAAGCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAG
ACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGAT
AGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCG
GACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGT
TTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATG
AGTGGTGGAACAGCTACTGGTGATGCCATTTCCTTCACTGTTAGAAATGTGTTTGGCCCT
ATAAGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGAT
GATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTGTTGGT
GTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTCAC
GCTTTCTTCACAAGAGAGTTCACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGC
ATTTGTAGAGATTTCTTAGAATCCCAGCAATAATGGTAACATTTTGACAACTGAAAGAAA
AAGTACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATA
CTAGAATCAGATACAAAACTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCC
TTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAG
GCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGAGATAATGTGGATTAAAACCTT
AAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAATTCCATAGCTCAATAAAAG
AATCTGATACTTAGACCAAAAAAAAAAA

FIGURE 82

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40604
><subunit 1 of 1, 550 aa, 0 stop
><MW: 59483, pI: 8.34, NX(S/T): 2
MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFS
VYGNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSAS
FTVTKGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRR
FNLQKNFVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGG
NSNTGKALKHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVS
VAKPIPEELGMVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSK
TCYNSVNIAFLIDGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFS
FTDYSTKENVLAVIRNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYD
DVQGPAAAAHDAGITIFSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRG
ICRDFLESQQ

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCCACCGCGCCGCTCCCGCATCTGCACCCGCAGC
CCGGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCA
GTCGGGGCGGCGGCTGCGGGCGCAGAGCGGAG
><MET {trans=1-s, dir=f, res=1}
ATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGGCGGCGGTCCCCACGGCC
CCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCGGCTCTCAGCTAC
CCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGATGGAGGAC
ACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTAAA
GCATCATCAGAAGTGAACCTGGCAAACTTACCTCCCAGCTATCACAATGAGACCAACACA
GACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAAC
AACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAA
GGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAG
TTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGG
GACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACC
AGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTGTGCTGT
GCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGAGCTT
TGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATGGA
GCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTG
CCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAG
CTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCC
GCCGCTGCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTG
CAATAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCT
TCTTCCTACATCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTG
CATTTGTTCAGCTCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTC
AGGCAGGGTTAAACTGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGC
CTCTACCAGTTGGCAGACAGCCGTTTGTTCTACATGGCTTTGATAATTGTTTGAGGGGAG
GAGATGGAAACAATGTGGAGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTG
CCCTGCTTTGCAAACATCAACCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCT
TTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCC
TGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGC
AGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTG
TTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCCCAAGTCA
CACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCTCT
CCACTACCCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGG
GATTTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACTAATTCTCACATCCCTCTA
AAAGTAAACTACTGTTAGGAACAGCAGTGTTCTCACAGTGTGGGGCAGCCGTCCTTCTAA
TGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTTGAAAGGT
ATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGG
CGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAACTGAAGACAATTATCAACC
ACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTTGTAATATGCGACTGCG
AACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTGTCATGGACTGTTGCCAC
CATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTATAAGCATGCTTT
CTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGCATAAATCACT
TCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMED
TQHKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITN
NQTGQMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTR
DSECCGDQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGEL
CHDPASRLLDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILL
PREVPDEYEVGSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

FIGURE 85A

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCT
CAGAAGGACTCTGAAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACA
CATGTGCATGTACACACACACATACACACACATACACCTTCCTCTCCTTCACTGAAGACTCA
CAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGACAGGCCTGG
CCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGGCCAGGCACGG
TGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAG
GAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAAATT
AGCCAGGAGTGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATC
GCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCGCTGCACTCCAGCCTGGGT
GACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGAGGGGTAGATACTGCTTCTCT
GCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGCCCCTGATGGGGCCTGGCAATGA
CTGAGCAGGCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
CGCCCGGTGTAGAATGACTGCCCTGGGAGGGTGGTTCCTTGGGCCCTGGCAGGGTTGCTGAC
CCTTACCCTGCAAAACACAAAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCC
TGCAGCTCCACCATGAGGCTTCTCGTGGCCCCACTCTTGCTAGCTTGGGTGGCTGGTGCCAC
TGCCACTGTGCCCGTGGTACCCTGGCATGTTCCCTGCCCCCCTCAGTGTGCCTGCCAGATCC
GGCCCTGGTATACGCCCCGCTCGTCCTACCGCGAGGCTACCACTGTGGACTGCAATGACCTA
TTCCTGACGGCAGTCCCCCCGGCACTCCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAA
CAGCATTGTCCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACC
TGTCCCAGAACAGCTTTTCGGATGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTG
ACCCTGCACCTAGAGGAGAACCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGC
CAGCCTACAGGAACTCTATCTCAACCACAACCAGCTCTACCGCATCGCCCCCAGGGCCTTTT
CTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGC
CGCTGGTTTGAAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGC
CATCCTGGACATGAACTTCCGGCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGA
ACCTGCGGGAGATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTC
TATGACAACCAGCTGGCCCGGGTGCCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTT
CCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGC
ACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTG
GTGAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
CCCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCA
GTGCCTTGCACCAGCAGACGGTGGAGTCCCTGCCCAACCTGCAGGAGGTAGGTCTCCACGGC
AACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCCAATGCCACGGGCACCCGTGTCCGCTT
CATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCCGGTCCGTG
AGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCTCATCTCCCCACGAAGCTTCCCC
CCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACC
CGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCA
GGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGTGACAGCAGAAGAGGCA
GGGCTATACACCTGTGTGGCCCAGAACCTGGTGGGGGCTGACACTAAGACGGTTAGTGTGGT
TGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCGGGTGC
AGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTCACCCCACCCAACACAGTGTCCACC
AACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCCT
GCCTCGGGGAACCCACAGCTACAACATTACCCGCCTCCTTCAGGCCACGGAGTACTGGGCCT
GCCTGCAAGTGGCCTTTGCTGATGCCCACACCCAGTTGGCTTGTGTATGGGCCAGGACCAAA
GAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCCTGGGCTCATTGCCATCCTGGCTCT
CGCTGTCCTTCTCCTGGCAGCTGGGCTAGCGGCCCACCTTGGCACAGGCCAACCCAGGAAGG
GTGTGGGTGGGAGGCGGCCTCTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCTTCT
GTCCGGGTTGTGTCTGCTCCCCTCGTCCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATC
CTCAGAAGGGGAGACACTGTTGCCACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTC
AGCAGTAGAGAAATCACTAGGACTACTTTTTACCAAAAGAGAAGCAGTCTGGGCCAGATGCC
CTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGG
GGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTC
ACCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCC

FIGURE 85B

TGCCTCCCCATCTTCTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGT
GTCCCCGGGCTGCACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGT
GCCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGT
GGGAGTGACCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATC
TCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGG
AGAAATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAA
TAAATAATAACAATAAAAAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLF
LTAVPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQ
LLSLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLL
RAIDSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGL
QSLESLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNM
EELVSIDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQT
VESLPNLQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPF
REMTDHCLPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGR
RYRVYPEGTLELRRVTAEEAGLYTCVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLEL
RVQETHPYHILLSWVIPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQA
TEYWACLQVAFADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAAH
LGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPP
LSQNS

FIGURE 87A

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGA
CATTGTGTACCGCCTCTAC
><MET {trans=1-s, dir=f, res=1}>
ATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTAC
TACGTGCACAACATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGC
TACCGCACCTACCGCTGTGCCCACCCCCTGGCCACACTCTTCAAGATCCTGGCGTCCTTC
TACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTACACACTGTGGTGGATGCTA
CGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAGCGAC
ATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCG
CTCTACTCCAAGCGCTTCGCCGTCTTCCTGTCGGAGGTGAGTGAGAACAAGCTGCGGCAG
CTGAACCTCAACAACGAGTGGACGCTGGACAAGCTCCGGCAGCGGCTCACCAAGAACGCG
CAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCATCCCTGACACTGTGTTTGAC
CTGGTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCCCAGC
ATTGCCCAGCTCACGGGCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAA
GCGCCTGCGCTGGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGAC
ATCAAGGAGATCCCGCTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACG
GGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGACGGGCTGCGGGAGCTCAAA
CGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCACAGAT
GTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCCTC
AACAGCCTCAAGAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAG
CGCATCCCCCACTCCATCTTCAGCCTCCACAACCTGCAGGAGATTGACCTCAAGGACAAC
AACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCTGCACCGCCTCACCTGCCTT
AAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAACCTG
GAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGC
CGCAAGCTGCGCTACCTGGACCTCAGCCACAACAACCTGACCTTCCTCCCTGCCGACATC
GGCCTCCTGCAGAACCTCCAGAACCTAGCCATCACGGCCAACCGGATCGAGACGCTCCCT
CCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCTGGGCAACAACGTGCTGCAG
TCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGGCAAC
CGGCTGGAGTGCCTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTG
GTGGTGGAGGAGGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGG
GCTGACAAGGAGCAGGCCTGAGCGAGGCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGC
CCAGTCCTCAGGCCCGGAGGGGCAGGCCTAGCTTCTCCCAGAACTCCCGGACAGCCAGGA
CAGCCTCGCGGCTGGGCAGGAGCCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGAGGAC
AGTATCTGTGGGGCTGGCCCCTTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGC
TTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGG
AGGCCAGCTCTGCCCCAGGGGCTGAGCTGCCACCAGAGGTCCTGGGACCCTCACTTTAGT
TCTTGGTATTTATTTTTCTCCATCTCCCACCTCCTTCATCCAGATAACTTATACATTCCC
AAGAAAGTTCAGCCCAGATGGAAGGTGTTCAGGGAAAGGTGGGCTGCCTTTTCCCCTTGT
CCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCG
GGGCGAACCAGCCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTC
CACGGGAGAGCAGGCCTCCAGCTGGAAAGGCCAGGCCTGGAGCTTGCCTCTTCAGTTTTT
GTGGCAGTTTTAGTTTTTTGTTTTTTTTTTTTTTAATCAAAAAACAATTTTTTTTAAAAA
AAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAAAAACTTAAAAAAAAAAA
GACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAG
CAGCCAGACGTTGAACTGTGTTTCCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGGA
TCTGGTGTGACCTTGGTCCAGGAGTTCTATTTGTTCCTGGGGAGGGAGGTTTTTTTGTTT
GTTTTTTGGGTTTTTTTGGTGTCTTGTTTTCTTTCTCCTCCATGTGTCTTGGCAGGCACT
CATTTCTGTGGCTGTCGGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAGACTC
GGGTTGGCTAATCCCCGGATGAACGGTGCTCCATTCGCACCTCCCCTCCTCGTGCCTGCC
CTGCCTCTCCACGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTT
CCCCACCTCCTGCGGCATGGGTGTGTCCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCA
GCCCTGTCGCCACCTGGTCCTTCATGAAGAGCAGACACTTAGAGGCTGGTCGGGAATGGG
GAGGTCGCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGCCTGG

FIGURE 87B

AGTGCACACAGCCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGG
GTCCCCACCTTAGAAGGGTCCCCGCCTTAGATCAATCACGTGGACACTAAGGCACGTTTT
AGAGTCTCTTGTCTTAATGATTATGTCCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCG
TCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGC
AAAAATCCGTTACATGTGGGTCTGAACTTGTAGACTCGGTCACAGTATCAAATAAAATCT
ATAACAGAAAAAAAAAAAAAAA

FIGURE 88

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35673
><subunit 1 of 1, 546 aa, 0 stop
><MW: 63742, pI: 8.62, NX(S/T): 6
MRQTIIKVIKFILIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASF
YISLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDP
LYSKRFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFD
LVELEVLKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTD
IKEIPLWIYSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTD
VGVHLQKLSINNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDN
NLKTIEEIISFQHLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYC
RKLRYLDLSHNNLTFLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQ
SLPSRVGELTNLTQIELRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWR
ADKEQA

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTC

><MET {trans=1-s, dir=f, res=1}

ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG

CTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACAGAGGAGGGCAAGGAAGTATGG

GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC

TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT

TCTAGCACTGGATTTGGAAACTTTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCA

CGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACT

GGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCA

GACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCA

TTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTT

TATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGAT

TCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCT

CTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCC

GTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATT

GAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAACTAAAAGCACTCCCACGTCT

ACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGCCAC

GTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAG

CTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAAC

ATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGG

ATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAG

GCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAG

GCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAAC

CTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATG

GCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGA

GCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCA

TTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGG

ATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAAACCTAA

GATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

><signal peptide>

MELALRRSPVPRWLLLLPLLLGLNA

><start mature protein>

GAVIDWPTEEGKEVW

><homology to peptidases 40-end>

DYVTVRKDAYMFWWLYYATNSCK

><potential N-glycosylation site>

NFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

GFSYV

><potential N-glycosylation site>

NGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELY

KAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVL

NAVNKGLYREATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCL

CQRHVRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIV

DELLEAGI

><potential N-glycosylation site>

NVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS

YKNLAFYWILKAGHMVPSDQGDMALKMMRLVTQQE

FIGURE 91

GGCCGCGGGAGAGGAGGCC

><MET {trans=1-s, dir=f, res=1}

ATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTCGGGCTGGACTCAGGAAG
CCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGACGGGTCATCACGTCG
CGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCAGGGGAGCCTGCGC
CTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGGCACTCACGGCG
GCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATGGTCCAGTTT
GGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCGTTACTTC
GTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTGCCTTG
GTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAGGCC
TCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAAA
GAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAAC
AACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGAC
ATGGTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGA
CCCTTGGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTG
GGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGG
ATCCAGAAGCTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTC
TTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCTACCTGAGCCCA
TGCAGCCTGGGGCCACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTTTGGTAATAA
ACACATTCCAGTTGATGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAA
A

FIGURE 92

><signal peptide>

MGARGALLLALLLARAGL

><start mature protein>

RKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWA

><Serine proteases, trypsin family, histidine active site 'LTAAHC'>

LTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRYLGNS

PYDIALVKLSAPVTYTKHIQPICLQASTFEFE

><potential N-glycosylation site>

NRTDCWVTGWGYIKEDEALPSPHTLQEVQVAII

><potential N-glycosylation site>

NNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNGLWYQIG

VVSWGVGCGRPNRPGVYT

><potential N-glycosylation site>

NISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPLLGPV

FIGURE 93

```
CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGA
<MET {trans=1-s, dir=f, res=1}
ATGGGACTCCAAGCCTGCCTCCTAGGGCTCTTTGCCCTCATCCTCTCTGGCAAATGCAGT
TACAGCCCGGAGCCCGACCAGCGGAGGACGCTGCCCCCAGGCTGGGTGTCCCTGGGCCGT
GCGGACCCTGAGGAAGAGCTGAGTCTCACCTTTGCCCTGAGACAGCAGAATGTGGAAAGA
CTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAGCTCTCCTCAATACGGAAAATACCTG
ACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCCCACTGACCCTCCACACGGTGCAA
AAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCTGTGATCACACAGGACTTTCTG
ACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCCTGGGGCTGAGTTTCATCAC
TATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCACATCCCTACCAGCTTCCA
CAGGCCTTGGCCCCCCATGTGGACTTTGTGGGGGGACTGCACCGTTTTCCCCCAACATCA
TCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCTGCATCTGGGGGTA
ACCCCCTCTGTGATCCGTAAGCGATACAACTTGACCTCACAAGACGTGGGCTCTGGCACC
AGCAATAACAGCCAAGCCTGTGCCCAGTTCCTGGAGCAGTATTTCCATGACTCAGACCTG
GCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGCCCGTGTG
GTTGGACAACAGGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGTACCTG
ATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAGGGA
CAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGTG
CATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTC
AACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCTGCTCTTCGCCTCAGGTGAC
AGTGGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCC
TCCAGCCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCACA
AATGAAATTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCA
TACCAGGAGGAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCCACCTGCCACCATCCAGT
TACTTCAATGCCAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGG
GTGGTCAGCAACAGAGTGCCCATTCCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTG
TTTGGGGGGATCCTATCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCCTCTT
GGCTTTCTCAACCCAAGGCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGT
GGCTGCCATGAGTCCTGTCTGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCCT
GGCTGGGATCCTGTAACAGGCTGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTAC
TCAACCCCTGACCCTTTCCTATCAGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAG
TTCAGTCCCTTATTCTGCCCTGTTGGAAGCCCTGCTGAACCCTCAACTATTGACTGCTGC
AGACAGCTTATCTCCCTAACCCTGAAATGCTGTGAGCTTGACTTGACTCCCAACCCTACC
ATGCTCCATCATACTCAGGTCTCCCTACTCCTGCCTTAGATTCCTCAATAAGATGCTGTA
ACTAGCATTTTTTGAATGCCTCTCCCTCCGCATCTCATCTTTCTCTTTTCAATCAGGCTT
TTCCAAAGGGTTGTATACAGACTCTGTGCACTATTTCACTTGATATTCATTCCCCAATTC
ACTGCAAGGAGACCTCTACTGTCACCGTTTACTCTTTCCTACCCTGACATCCAGAAACAA
TGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATGGCCTTTCCATCATAGTTGCCCAC
TCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTGACTACTCTTGTCTTCCTCTCT
CATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGCTCCATTTGTAGATTTTTGC
TCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACATCTACAACCATTACCAT
CTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAATGTAAAAAA
```

FIGURE 94

><signal peptide>

MGLQACLLGLFALILS

><start mature protein>

GKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLSELVQAVSDPSSP
QYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWLSIRQAEL
LLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRPEPQ
VTGTVGLHLGVTPSVIRKRY

><potential N-glycosylation site>

NLTSQDVGSGTS

><potential N-glycosylation site>

NNSQACAQFLEQYFHDSDLAQFMRLFGGNFAHQASVARVVGQQGRGRAGIEASLDV
QYLMSAGA

><potential N-glycosylation site>

NISTWVYSSPGRHEGQEPFLQWLMLLS

><potential N-glycosylation site>

NESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVS
GRHQFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKF
LSSSPHLPPSSYF

><potential N-glycosylation site>

NASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSGRPPL
GFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

FIGURE 95

GCCGCGCGCTCTCTCCCGGCGCCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGG
GCGGGCTGCTCGGCGCGGAACAGTGCTCGGC
><MET {trans=1-s, dir=f, res=1}>
ATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTCTTCTTTCTGCTCTGTGCTGTTGGGCAA
GTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTGGCCTGCATACCGCCTCCCTGTCGTC
TTGCCCCAGTCTACCCTCAATTTAGCCAAGCCAGACTTTGGAGCCGAAGCCAAATTAGAA
GTATCTTCTTCATGTGGACCCCAGTGTCATAAGGGAACTCCACTGCCCACTTACGAAGAG
GCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGGCAGCCGCACAGAGACGCAG
GTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAACACCGAGACTCAGGGTCT
TCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGCAGGTTCAGCATTTTT
GGGAAGGACTTCCTGCTCAACTACCCTTTCTCAACATCAGTGAAGTTATCCACGGGCTGC
ACCGGCACCCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCCACTGCATACACGATGGA
AAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCCAAGTTTAAA
GATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAAATTTCAG
TGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCAATGAC
ATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAATTT
ATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACTTCTCT
GGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAG
ACCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTC
TATGTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTT
TCAGGGCACCAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTCAGA
ATCACTCCTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAAACTACCTGGATTGT
AGGGAGGGGTGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTT
TAGGAGAGGCCAAATTGTTTTTTGTCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGT
GTGTGTAAGGTGTCTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTT
ACTATTTGAAAACTGGTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATA
CTTTTGCATAGAAATAAAAAAAATACTGATTTGGGGCAATGAGGAATATTTGACAATTAA
GTTAATCTTCACGTTTTTGCAAACTTTGATTTTTATTTCATCTGAACTTGTTTCAAAGAT
TTATATTAAATATTTGGCATACAAGAGATATGAAAAAAAAAAAAAAA

FIGURE 96

><signal peptide>

MAGIPGLLFLLFFLLCAVG

><start mature protein>

QVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSSSCGPQCHKGTPLP

TYEEAKQYLSYETLYA

><potential N-glycosylation site>

NGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRRKRQIYGYDSRFSIFGKDFLLNYPFS

TSVKLSTGCTGTLVAEKHV

><serine proteases, trypsin family, histidine active site 'LTAAHC'>

LTAAHCIHDGKTYVKGTQKLRVGFLKPKFKDGGRGA

><potential N-glycosylation site>

NDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLELKKPHKRKFM

KIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGASGS

GVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIK

GNYLDCREG

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCCGCCCCACCAGCC

><MET {trans=1-s, dir=f, res=1}

ATGGTGGTTTCTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCC

CTGCTGCTGCTGGCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCC

TGTGGGAAGCCCCAGCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAG

TGGCCCTGGATCGTGAGCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTC

ACCAGCCGCTGGGTGATCACTGCTGCCCACTGTTTCAAGGACAACCTGAACAAACCATAC

CTGTTCTCTGTGCTGCTGGGGGCCTGGCAGCTGGGGAACCCTGGCTCTCGGTCCCAGAAG

GTGGGTGTTGCCTGGGTGGAGCCCCACCCTGTGTATTCCTGGAAGGAAGGTGCCTGTGCA

GACATTGCCCTGGTGCGTCTCGAGCGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATC

TGCCTACCTGATGCCTCTATCCACCTCCCTCCAAACACCCACTGCTGGATCTCAGGCTGG

GGGAGCATCCAAGATGGAGTTCCCTTGCCCCACCCTCAGACCCTGCAGAAGCTGAAGGTT

CCTATCATCGACTCGGAAGTCTGCAGCCATCTGTACTGGCGGGGAGCAGGACAGGGACCC

ATCACTGAGGACATGCTGTGTGCCGGCTACTTGGAGGGGGAGCGGGATGCTTGTCTGGGC

GACTCCGGGGGCCCCCTCATGTGCCAGGTGGACGGCGCCTGGCTGCTGGCCGGCATCATC

AGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCCGGGGTCTACATCAGCCTCTCTGCG

CACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCAGCTCCGCGGGCGCGCTCAGGGG

GGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCGCCGCGCGCTCCTAGGGCGCA

GCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACATCTGGATCTGGATCTGCG

GCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACCTCTACCTCTGGGGGCC

CGGACGGCTGCTGCGGAAAGGAAACCCCCTCCCCGACCCGCCCGACGGCCTCAGGCCCCC

CTCCAAGGCATCAGGCCCCGCCCAACGGCCTCATGTCCCCGCCCCCACGACTTCCGGCCC

CGCCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTATAGGTATTTGT

AACCCTGCCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATTCTCCAAAA

AAAAAA

FIGURE 98

><signal peptide>

MVVSGAPPALGGGCLGTFTSLLLLASTAILNA

><start mature peptide>

ARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQK

><potential N-glycosylation site>

NGTHHCAGSLLTSRWV

><Serine proteases active site ITAAHC>

ITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVAWVEPHPVYSWKEGACA

DIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDGVPLPHPQTLQKLKV

PIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMCQVDGAWLL

AGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQGSGA

AARS

FIGURE 99

GACGGCTGGCCACC
><MET {trans=1-s, dir=f, res=1}
ATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTACTGCTGGTGGCC
ACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGTGGAGCTGCAC
AACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGAGATGGGAC
GAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCACAACAAG
GAGCGCGGGCGCCGCGGCGAGAATCTGTTCGCCATCACAGACGAGGGCATGGACGTGCCG
CTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCTGC
AGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTTGAGGAGACCAACATCGAATTA
CTGGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGG
ACTCCGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATC
GGAAGCCCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGG
GCGACTGAAGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATT
CCGGCTTTCTTGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTG
GAAACCCAGGCCCCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCT
CCACCTTGCGTAACAACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTG
GATGAGGAGCCAGTTACCTTCCCCAAATCGACCCATGTTCCTATCCCAAAATCAGCAGAC
AAAGTGACAGACAAAACAAAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAG
ATCTCCCTGACAGGGGCAAGGGAACTCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAG
GCTGAGTTGCCTCCTTCCAGTGAGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCA
GGTGAGCTGCAGGCCACACTGGACCACACGGGGCACACCTCCTCCAAGTCCCTGCCCAAT
TTCCCCAATACCTCTGCCACCGCTAATGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCG
TCCTTGCCAGGTGCAGAGGGCCCTGACAAGCCTAGCGTTGTGTCAGGGCTGAACTCGGGC
CCTGGTCATGTGTGGGGCCCTCTCCTGGGACTACTGCTCCTGCCTCCTCTGGTGTTGGCT
GGAATCTTCTGAATGGGATACCACTCAAAGGGTGAAGAGGTCAGCTGTCCTCCTGTCATC
TTCCCCACCCTGTCCCCAGCCCCTAAACAAGATACTTCTTGGTTAAGGCCCTCCGGAAGG
GAAAGGCTACGGGGCATGTGCCTCATCACACCATCCATCCTGGAGGCACAAGGCCTGGCT
GGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACCGGGCCCACACCTCTCCTGCCCC
TCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCTCACTGCCTACCTGGCCTGGG
GCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTGTGTAGCTGGGGATGGGGA
TTCCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTCTTTGAGTGGGGGAGGC
AGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCTGTCCAACCTGTGAA
A

FIGURE 100

><signal peptide>

MHGSCSFLMLLLPLLLLLVATT

><start of mature peptide, extracellular domain>

GPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEELAAFAKAYARQCVW

GHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHY

><potential N-glycosylation site>

NLSAATCSPGQMC

><GHYTQVVWAKT Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1 - CRISP signature>

GHYTQVVWAKTERIGCGSHFCEKLQGVEETNIEL

><LLVCNYEPPGNV Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2 -CRISP signature>

LVCNYEPPGNVKGKRPYQEGTPCSQCPSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFR

ATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEA

PPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPIPKSADKVTDKTKVPSRSPENSLDPK

MSLTGARELLPHAQEEAEAEAELPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSLPN

FP

><potential N-glycosylation site>

NTSATA

><potential N-glycosylation site>

NATGGRALALQSSLPGAEGPDKPSVVSGLNS

><potential glycosylphosphatidylinositol attachment site>

GPGHVWGPLLGLLLLPPLVLAGIF

FIGURE 101A

GTAACTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCA
AGTT
><MET {trans=1-s, dir=f, res=1}
ATGGTGGACGTACTTCTGTTGTTCTCCCTCTGCTTGCTTTTTCACATTAGCAGACCGGAC
TTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTT
CGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCG
GCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACAT
CTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTC
CAAACTGCATTTCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACA
TCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAAC
AGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTC
GAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCT
CTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTGG
GGGCTGAGCAACATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAA
GGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACTTCATCTCAGCCAAAATGCCATCAAC
AGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTAACTTTC
AATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTG
CACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGT
TTAAAGACTTTGGATCTGAAGAACAATGAAATTTCCTGGACTATTGAAGACATGAATGGT
GCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCCAAGGAAATCGGATCCGTTCT
ATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGTGACAAC
GCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAAACTGCAACAATTGCAT
TTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGGGTGGCG
GAAAACAACTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGA
AGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCCCAAACCCCAG
ATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTCATCTGC
TCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAAGACAATGAACTA
CTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATG
GAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAG
TGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
ATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCA
CGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCCAGATAGCCTGGCAGAAGGATGGG
GGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTG
TTCTTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAAC
AGTGCAGGAAGTATTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTG
CGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCT
GGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACC
GAGAGGCACTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGT
GATGCTGGGAAATACACATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTG
CGCCTCAGTGTGATCCCCACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTA
GACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTG
GGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGC
AGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCATCT
CAGGGAACGTTAGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCAC
CAGTTTGTCACATCTTCAGGTGCTGGATTTTTCTTACCACAACATGACAGTAGTGGGACC
TGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTCCTTTGT
CCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCT
TTTGAAACATATCATACAGGTTGCAGTCCTGACCCAAGAACAGTTTTAATGGACCACTAT
GAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCC
TGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACATGTGAGGAAGCTACTTAACACT
AGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCCTCTTTA
GATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTCTTTCATGGGTACC
TTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCA

FIGURE 101B

GATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGG
TCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCACATTTGTACCTTT
AAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTGGACACATAG
ACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTATTTAAAAG
AGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAATGCTTTA
TTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTTATACTGGGAATGATGC
TCATATAAGAATACCTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTATCTT
ACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGCCAGATTTCTT
TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAA
ATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT
SMEPGYFDNLANTLLVLKLNRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
RISPDAWEFCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSS
LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKG
RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEL
LHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDV
FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIA
GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNV
RLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDC
SITNTDETNLPADIPSYLSSQGTLADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLKGNVYGSDPFETYHTGCSPDPRTVLMDHY
EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMRNLCLNKSSL
DFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDSG
SEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGG
TGCCTTGCAAAAATGAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGAT
AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTTTCTTGTGAGCCCTGGATCTTA
ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACCAGAGTTAGA
CCCGCGGGGGTTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGT
ATGTTCATTTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAG
TTTGGGGCTTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTTTCCTTTCTTTTTGAA
TTTCCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAATTTCAGAGAAGAAAA
GTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACC
TCCTTTTTTTCAAATTTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTTCTT
AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACTGTTTGAAT
TCCAGAAGGACCAACACCAGATAAATTATGA
><MET {trans=1-s, dir=f, res=1}
ATGTTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAACAGG
GCCCTATTTGACCCCCTGCTTGTGGTGCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGT
CTGGTGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTG
ATTTGTGTTCGGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCAACACACGGCTG
CTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGG
CACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTC
AATGGTCTGGCGAACCTCAACACTCTGGAACTCTTTGACAATCGTCTTACTACCATCCCG
AATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTTGCGAAACAACCCCATT
GAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTTGCGCCGACTAGACTTAGGG
GAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACTTGAGG
TATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAAA
CTAGATGAGCTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAG
GGTTTGATGCACCTTCAAAAACTGTGGATGATACAGTCCCAGATTCAAGTGATTGAACGG
AATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACA
TTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCAC
AACCCTTGGAACTGTAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCC
CCCTCGAACACAGCTTGTTGTGCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTAC
ATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCT
GCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATCC
CTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAA
GTGCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCACAAATGTAACTGTGCAAGAT
ACAGGCATGTACACATGTATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACC
CTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTCAACCGTCACAGTAGAG
ACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCCA
GTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTCG
ACAGAGAAAACCTTCACCATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGAT
GAGGTCATGAAGACTACCAAAATCATCATTGGGTGTTTTGTGGCCATCACACTCATGGCT
GCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAC
GCCCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCC
ATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCA
TACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCAATACACAGTTCA
GTGCATGAACCGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATC
TAAAACATTTACAGAGTTACAAAAAACAAACAATCAAAAAAAAAAGACAGTTTATTAAAAA
TGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAAACAAA
AAAGAAAAGAAATTTATTTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

><signal peptide>

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVVAGLVRA

><start mature peptide, extracellular domain>

QTCPSVCSCSNQFSKVICVRKNLREVPDGISTNTRL

><start leucine rich repeat domains>

LNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLANLNTLELFDNRLTTIPN

GAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLSYISEGAFEGLSNLRY

LNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKLWMIQSQIQVIER

NAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCDILWLSWWIK

DMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAELK

CRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSN

SVGNTTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWE

><end leucine rich repeat domains>

TTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDE

><start transmembrane domain>

VMKTTKIIIGCFVAITLMAAVMLVI

><start intracellular domain>

FYKMRKQHHRQNHHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYNSYKS

PFNHTTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

FIGURE 105A

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTG
CTGTTTGGGGGCATGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCG
CGAGGGAGGAGCGCGCACGCGACCGCGAGGGCGGGCGTGCACCCTCGGCTGGAAGTTTGTGC
CGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTAGAGACCTAGGCCGCTGGACCGCGAT
GAGCGCGCCGAGCCTCCGTGCGCGCGCCGCGGGGTTGGGGCTGCTGCTGTGCGCGGTGCTGG
GGCGCGCTGGCCGGTCCGACAGCGGCGGTCGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCC
GCCGAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAA
GCGGCTAGCGCGTCTTCCCGAGCCACTCCCGTCCTGGGTCGCTCGGCTGGACTTAAGTCACA
ACAGATTATCTTTCATCAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAA
CTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCAGTCTCGGCAAATATTACACT
TCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAGTTTCAGT
CCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATTTCCAGCC
CTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTT
TGACAATTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCC
CACCCAAGATGTTTAAACTGCCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTAAA
AATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCTCTGAAAATGCAAAGAAA
TGGAGTAACGAAACTTATGGATGGAGCTTTTTGGGGGCTGAGCAACATGGAAATTTTGCAGC
TGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAG
GAACTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCA
GAAGCTCAGTGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCC
TLGCCCTAAGCTTACTAAATACACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGAT
TGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAACAATGAAATTTCCTG
GACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTCC
AAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCAT
CTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAA
ACTGCAACAATTGCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCC
CACAGTGGGTGGCGGAAAACAACTTTCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAG
CTGCTAAAAGGAAGAAGCATTTTTGCTGTTAGCCCAGATGGCTTTGTGTGTGATGATTTTCC
CAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTT
TCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGCTTGGAAAAAAGACAAT
GAACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGT
GATGGAGTATACCACCATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATC
AGTGTGTCATCTCCAATCACTTTGGTTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAAT
ATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCCATGGCACG
CTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCCAGATAGCCTGGCAGAAGGATGGGGGCA
CAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTT
ATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGG
AAGTATTTCAGCAAATGCAACTCTGACTGTCCTAGAAACACCATCATTTTTGCGGCCACTGT
TGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGCATTGCTGGAGGAAGCCCT
CCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCACTTTTT
TGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACA
CATGTGAGATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCC
ACTCCAACCTGCGACTCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCAC
TGTGGGTGTCGTGATCATAGCCGTGGTTTGCTGTGTGGTGGGCACGTCACTCGTGTGGGTGG
TCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACCAACACAGATGAGACC
AACTTGCCAGCAGATATTCCTAGTTATTTGTCATCTCAGGGAACGTTAGCTGACAGGCAGGA
TGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACCAGTTTGTCACATCTTCAGGTGCTGGAT
TTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGAT
GTGGAAGCTGCCACAGATCTGTTCCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTT
GAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACATATCATACAGGTTGCAGTCCTGACC
CAAGAACAGTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAGGAGTGCTACCCA
TGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACA
TGTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGT
GTCTAAACAAGTCCTCTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTCGGTTGCCTCGAGT
AATTCTTTCATGGGTACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAG

FIGURE 105B

CTTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAG
ACTTGGACTCTGGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAAGAAAATCAC
ATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTT
GGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACTTTTA
TTTAAAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAT
GCTTTATTTATACAGATGAACCAAAATTACAAAAAGTTATGAAAATTTTTATACTGGGAATG
ATGCTCATATAAGAATACCTTTTTAAACTATTTTTTAACTTTGTTTTATGCAAAAAAGTATC
TTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTATAATGCCAGATTTCTT
TTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAAT
AGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA

FIGURE 106

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA37140
><subunit 1 of 1, 1119 aa, 1 stop
><MW: 123434, pI: 6.09, NX(S/T): 12

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDC
SRKRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVS
ANITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVT
SMEPGYFDNLANTLLVLKLNRNRISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGA
LKSLKMQRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIN
RISPDAWEFCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSS
LKTLDLKNNEISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDN
AIMSLQGNAFSQMKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKG
RSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEL
LHDAEMENYAHLRAQGGEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVN
MLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDV
FFIVDVKIEDIGVYSCTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIA
GGSPPPKLNWTKDDSPLVVTERHFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNV
RLSVIPTPTCDSPQMTAPSLDDDGWATVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDC
SITNTDETNLPADIPSYLSSQGTLADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGT
CHIDNSSEADVEAATDLFLCPFLGSTGPMYLKGNVYGSDPFETYHTGCSPDPRTVLMDHY
EPSYIKKKECYPCSHPSEESCERSFSNISWPSHVRKLLNTSYSHNEGPGMKNLCLNKSSL
DFSANPEPASVASSNSFMGTFGKALRRPHLDAYSSFGQPSDCQPRAFYLKAHSSPDLDSG
SEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

FIGURE 107A

CAAAACTTGCGTCGCGGAGAGCGCCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGA
GCGCAGCTGAGACTGGGGGAGCGCGTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAG
CAGGGAAGGGGAAGCTGTGGTCTGCCCTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGA
GCCCCTGGGTGGTCCCGTCCCCTATCCCTCCTTTATATAGAAACCTTCCACACTGGGAAGGC
AGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAGGCGCACAGCA
TTCCGAGTTTACAGATTTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCT
GGTTCCATCAGCCCTGGCGCCCAGGCGCATCTGACTCGGCACCCCCTGCAGGCACCATGGCC
CAGAGCCGGGTGCTGCTGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCT
TGCCGTGAGGGCCCCAGGATTTGGCCGAAGTGGCGGCCACAGCCTGAGCCCCGAAGAGAACG
AATTTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGGAGCCCGGGCCTGGCCCAGCC
GCGGTCAGCTGCCCCCGAGACTGTGCCTGTTCCCAGGAGGGCGTCGTGGACTGTGGCGGTAT
TGACCTGCGTGAGTTCCCGGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACA
ACCAGCTGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAAC
CTGCAAAACAACCGCCTGACTTCCCGAGGGCTCCCAGAGAAGGCGTTTGAGCATCTGACCAA
CCTCAATTACCTGTACTTGGCCAATAACAAGCTGACCTTGGCACCCCGCTTCCTGCCAAACG
CCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCTATGGGCTCACCTTTGGC
CAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGCTGCC
GGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCCTCATCCTGTCCAGCAACTTCCTGC
GCCACGTGCCCAAGCACCTGCCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTG
GAGAAGATCCCCCCGGGGGCCTTCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAA
CAACTACCTGACTGACGAGGGCCTGGACAACGAGACCTTCTGGAAGCTCTCCAGCCTGGAGT
ACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGCCGCGCAGCCTGGTG
CTGCTGCACTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCCG
CAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGG
CCTTCCAGGGCCTCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTG
CCCAGTGGCCTGCCTCGCCGCGTGCGCACCCTCATGATCCTGCACAACCAGATCACAGGCAT
TGGCCGCGAAGACTTTGCCACCACCTACTTCCTGGAGGAGCTCAACCTCAGCTACAACCGCA
TCACCAGCCCACAGGTGCACCGCGACGCCTTCCGCAAGCTGCGCCTGCTGCGCTCGCTGGAC
CTGTCGGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAA
GGTCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGC
GTGAGCTGTACCTCACCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTG
GACCTCGCCCATCTGCAGCTGCTGGACATCGCCGGGAATCAGCTCACAGAGATCCCCGAGGG
GCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAACAAGATTAGTGCGGTGCCCGCCA
ATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGCTGGCTGTG
GGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGG
CAACTTAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGG
AGGAAGAGGAGGAGGAGGAGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACC
TAGGATGATGGACCGCCGGACTCTTTTCTGCAGCACACGCCTGTGTGCTGTGAGCCCCCCAC
TCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCATCCCACATGACACGGGCT
GACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGCACACA
CATCACACCCTCAAACACCCAGCTCAGCCACACACAACTACCCTCCAAACCACCACAGTCTC
TGTCACACCCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCTGC
CCTGGCACACACAGGCACCCATTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACA
CCACACACACACACATGCACAAGTCATGTGCGAACAGCCCTCCAAAGCCTATGCCACAGACA
GCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCTGTCCATCTGTCCGTC
CGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCTGG
AACTCACAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTG
CTGGCCTGGCCTGGCCCACCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCC
TCCCTGCCACGCCCTGGCAGGACACAGGCACTTTTCCAATGGGCAAGCCCAGTGGAGGCAGG
ATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGGCAGGAGTGAAGCAGAGGTGATGGGG

FIGURE 107B

CTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTTGTTCTTCAGGCC
TGTGGGGGAAGTTCCGGGTGCCTTTATTTTTTATTCTTTTCTAAGGAAAAAAATGATAAAAA
TCTCAAAGCTGATTTTTCTTGTTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGC
AAAAAAAAAA

FIGURE 108

Met Glu Gly Glu Glu Ala Glu Gln Pro Ala Trp Phe His Gln Pro Trp
Arg Pro Gly Ala Ser Asp Ser Ala Pro Pro Ala Gly Thr Met Ala Gln
Ser Arg Val Leu Leu Leu Leu Leu Leu Leu Leu Pro Pro Gln Leu His Leu
Gly Pro Val Leu Ala Val Arg Ala Pro Gly Phe Gly Arg Ser Gly Gly
His Ser Leu Ser Pro Glu Glu Asn Glu Phe Ala Glu Glu Glu Pro Val
Leu Val Leu Ser Pro Glu Glu Pro Gly Pro Gly Pro Ala Ala Val Ser
Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val Val Asp Cys Gly
Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro Glu His Thr Asn
His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile Tyr Pro Glu Glu
Leu Ser Arg Leu His Arg Leu Glu Thr Leu Asn Leu Gln Asn Asn Arg
Leu Thr Ser Arg Gly Leu Pro Glu Lys Ala Phe Glu His Leu Thr Asn
Leu Asn Tyr Leu Tyr Leu Ala Asn Asn Lys Leu Thr Leu Ala Pro Arg
Phe Leu Pro Asn Ala Leu Ile Ser Val Asp Phe Ala Ala Asn Tyr Leu
Thr Lys Ile Tyr Gly Leu Thr Phe Gly Gln Lys Pro Asn Leu Arg Ser
Val Tyr Leu His Asn Asn Lys Leu Ala Asp Ala Gly Leu Pro Asp Asn
Met Phe Asn Gly Ser Ser Asn Val Glu Val Leu Ile Leu Ser Ser Asn
Phe Leu Arg His Val Pro Lys His Leu Pro Pro Ala Leu Tyr Lys Leu
His Leu Lys Asn Asn Lys Leu Glu Lys Ile Pro Pro Gly Ala Phe Ser
Glu Leu Ser Ser Leu Arg Glu Leu Tyr Leu Gln Asn Asn Tyr Leu Thr
Asp Glu Gly Leu Asp Asn Glu Thr Phe Trp Lys Leu Ser Ser Leu Glu
Tyr Leu Asp Leu Ser Ser Asn Asn Leu Ser Arg Val Pro Ala Gly Leu
Pro Arg Ser Leu Val Leu Leu His Leu Glu Lys Asn Ala Ile Arg Ser
Val Asp Ala Asn Val Leu Thr Pro Ile Arg Ser Leu Glu Tyr Leu Leu
Leu His Ser Asn Gln Leu Arg Glu Gln Gly Ile His Pro Leu Ala Phe
Gln Gly Leu Lys Arg Leu His Thr Val His Leu Tyr Asn Asn Ala Leu
Glu Arg Val Pro Ser Gly Leu Pro Arg Arg Val Arg Thr Leu Met Ile
Leu His Asn Gln Ile Thr Gly Ile Gly Arg Glu Asp Phe Ala Thr Thr
Tyr Phe Leu Glu Glu Leu Asn Leu Ser Tyr Asn Arg Ile Thr Ser Pro
Gln Val His Arg Asp Ala Phe Arg Lys Leu Arg Leu Leu Arg Ser Leu
Asp Leu Ser Gly Asn Arg Leu His Thr Leu Pro Pro Gly Leu Pro Arg
Asn Val His Val Leu Lys Val Lys Arg Asn Glu Leu Ala Ala Leu Ala
Arg Gly Ala Leu Ala Gly Met Ala Gln Leu Arg Glu Leu Tyr Leu Thr
Ser Asn Arg Leu Arg Ser Arg Ala Leu Gly Pro Arg Ala Trp Val Asp
Leu Ala His Leu Gln Leu Leu Asp Ile Ala Gly Asn Gln Leu Thr Glu
Ile Pro Glu Gly Leu Pro Glu Ser Leu Glu Tyr Leu Tyr Leu Gln Asn
Asn Lys Ile Ser Ala Val Pro Ala Asn Ala Phe Asp Ser Thr Pro Asn
Leu Lys Gly Ile Phe Leu Arg Phe Asn Lys Leu Ala Val Gly Ser Val
Val Asp Ser Ala Phe Arg Arg Leu Lys His Leu Gln Val Leu Asp Ile
Glu Gly Asn Leu Glu Phe Gly Asp Ile Ser Lys Asp Arg Gly Arg Leu
Gly Lys Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
Thr Arg

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTC
CTCCGGGAGCGGCAGCAGTAGCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAG
AGGGGCGCCTCCCATCGGCGCCCACCACCCCAACCTGTTCCTCGCGCGCCACTGCGCTGC
GCCCCAGGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGTGCTGGTATCCTCGCT
CTACCTGCAGGCGGCCGCCGAGTTCGACGGGAGGTGGCCCAGGCAAATAGTGTCATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTG
GGGACAGTGTCAGCCTGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAA
CAAGTGCAAGTGTCATCCTGGTTATGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTG
TGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTACGGCAGCTACAAGTG
CTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTG
CCCATCCCCTGGCCTGCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATG
TGCTACAGGAAGAGCCTCCTGCCCTAGATTTAGGCAATGTGTCAACACTTTTGGGAGCTA
CATCTGCAAGTGTCATAAAGGCTTCGATCTCATGTATATTGGAGGCAAATATCAATGTCA
TGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCCTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTG
TGTGTATATCCCAAAAGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAAA
TGGTACCATTTTAAAGGGTGACACAGGAAATAATAATTGGATTCCTGATGTTGGAAGTAC
TTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAACAGGCCTACTTCTAA
GCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCCAGAAAGGCCAACCACCGG
ACTGACAACTATAGCACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAG
GGTACAGACAGACCCTCAGAAACCCAGAGGAGATGTGTTCAGTGTTCTGGTACACAGTTG
TAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAATGACTTGCACTGGGA
ACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTCGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCCTCATGCATTCAGGGGACCTGTG
CCTGTCATTCAGGCACAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAG
AAAACACGGTGCCCACGGAGCAGCCCTGTGGGGAAGAAATGGTGGCCATGGCTGGAGGCA
AACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGAATCACAAAGATGATTAAAGGG
TTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAG
GGTGGCGACCAGCTGTTCTCCATATGCACTAAGAATAGAACAAGAGGAAACTGGCTTAGA
CTAGAGTATAAGGGAGCATTTCTTGGCAGGGGCCATTGTTAGAATACTTCATAAAAAAAG
AAGTGTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGATAAAAATTTGTCTAT
TTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGAC
AAGGCTTAATTTAGGCATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAG
AGCCCACCAAATGCTGAGCTCACTGAAATATCTCTCCCTTATGGCAATCCTAGCAGTATT
AAAGAAAAAAGGAAACTATTTATTCCAAATGAGAGTATGATGGACAGATATTTTAGTATC
TCAGTAATGTCCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTAAGAGATCCTTCAAGGA
ACACAGTTCAGAGAGATTTTCATCGGGTGCATTCTCTCTGCTTCGTGTGTGACAAGTTAT
CTTGGCTGCTGAGAAAGAGTGCCCTGCCCCACACCGGCAGACCTTTCCTTCACCTCATCA
GTATGATTCAGTTTCTCTTATCAATTGGACTCTCCCAGGTTCCACAGAACAGTAATATTT
TTTGAACAATAGGTACAATAGAAGGTCTTCTGTCATTTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCAT
TTTTAATGGTTCATTTCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAA
ATAAATGAAAATTTTACTTTTCGATGCCAATGATACATTGCACTAAACTGATGGAAGAAG
TTATCCAAAGTACTGTATAACATCTTGTTTATTATTTAATGTTTTCTAAAATAAAAAATG
TTAGTGGTTTTCCAAATGGCCTAATAAAAACAATTATTTGTAAATAAAAACACTGTTAGT
AAT

FIGURE 110

><signal peptide>
MDFLLALVLVSSLYLQA
><start mature protein>
AAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPV
><EGF-like repeats, 60-253>
CQPRCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYML
MPDGSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPRF
RQCVNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEG
YQGDGLTCVYIPKVMIEPSGPIHVPKG
><potential N-glycosylation site>
NGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRPTSKPTTRPTPKPTPIPTPPPPPPL
PTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDNRVQTDPQKPRGDVFSVLVHSCNFD
HGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPLGRLMHSGDLCLSFRH
KVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSESQR

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTTCCTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT
ATATCCATGTGTCTTCTCTTCCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACTTTCATGG
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTCGATTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTCACAAAAACAAAACTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTA
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAAAAAAAAA

FIGURE 112

Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly Ala
Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His Gly Val
Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe His Thr Pro
Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg Pro His Thr Met
Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser Val Val Pro Asp Leu
Glu Tyr Gln His Lys Phe Thr Met Met Pro Pro Asn Ala Ser Leu Leu
Ile Asn Pro Leu Gln Phe Pro Asp Glu Gly Asn Tyr Ile Val Lys Val
Asn Ile Gln Gly Asn Gly Thr Leu Ser Ala Ser Gln Lys Ile Gln Val
Thr Val Asp Asp Pro Val Thr Lys Pro Val Val Gln Ile His Pro Pro
Ser Gly Ala Val Glu Tyr Val Gly Asn Met Thr Leu Thr Cys His Val
Glu Gly Gly Thr Arg Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro
Val His Thr Ser Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu
His Ile Ala Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu
Val Arg Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile
Ile Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu Phe
Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp Ile Arg
Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro Arg Leu Glu
Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp Tyr Val Cys Cys
Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu Thr His Phe Thr Val
Ile Ile Thr Ser Val Gly Leu Glu Lys Leu Ala Gln Lys Gly Lys Ser
Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile Ser Leu Phe Leu Ile Ile
Ser Met Cys Leu Leu Phe Leu Trp Lys Lys Tyr Gln Pro Tyr Lys Val
Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu Thr Glu Tyr Arg Lys Ala
Gln Thr Phe Ser Gly His Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr
Glu Phe Val Ala Phe Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser
Arg Ser Val Pro Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser
Thr Val Tyr Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His
Pro Glu

FIGURE 113

GCAAGCGGCGAA
><MET {trans=1-s, dir=f, res=1}
ATGGCGCCCTCCGGGAGTCTTGCAGTTCCCCTGGCAGTCCTGGTGCTGTTGCTTTGGGGT
GCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCGCGTCATCACGGACGAGAACTGGAGA
GAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGTCAA
AATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAATATT
GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTT
CCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCA
TGGTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATG
TGGATCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCA
TATACTGTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATA
TTTGTGGCAGATTGCCTTTGTCCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCT
TCAAAAAAATTATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAG
GCGGATGAAGAAGATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGAC
TTTCCACAGAATGCCATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCC
TAGTTAAATTTTATAGTTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCAT
TTTGTTTGGTTTGAAGTGAACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTG
TCATTAAATTGAAGAGTCTACATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAAT
ATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAA
GCAATAAGATTTATGTATATTTGTTTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAA
TTTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATTATTTTAGAGAAAAAT
ATTTCTCATTTGATATAATTTTTCTCTGTTTCACTGTGTGAAAAAAAGAAGATATTTCCC
ATAAATGGGAAGTTTGCCCATTGTCTCAAGAAATGTGTATTTCAGTGACAATTTCGTGGT
CTTTTTAGAGGTATATTCCAAAATTTCCTTGTATTTTTAGGTTATGCAACTAATAAAAAC
TACCTTACATTAATTAATTACAGTTTTCTACACATGGTAATACAGGATATGCTACTGATT
TAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT
ATTTTTCTTACTTACTATGGGTTACATTTTTTATTTTTCAAATTGGATGATAATTTCTTG
GAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTTGTTTCAAACTGAAGTTTACT
GAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAATTTTGGCCACTTTTTTCAGA
TTTTACATCATTCTTGCTGAACTTCAACTTGAAATTGTTTTTTTTTTCCTTTTGGATGTG
AAGGTGAACATTCCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAA
AATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAGCATCTTCTTGTA
TATGTCTTAAATGTATTTTTGTCCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCT
GTAATGCTTGATGTTTTAAAATAATAACATTTTTATATTTTTTAAAAGACAAACTTCATA
TTATCCTGTGTTCTTTCCTGACTGGTAATATTGTGTGGGATTTCACAGGTAAAAGTCAGT
AGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTTCACC
TTAAAAGAAGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGACAA
TTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAAATATTGTACCA
TTAAAGAGTTTGGATGTGTAACTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAA
ACCTTTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQ
NLQPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTK
KDFINFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGS
YTVFALATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQE
ADEEDVSEEEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCC
TTCTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAG
CGGGAAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACC
><MET {trans=1-s, dir=f, res=1}
ATGAAACTCTGGGTGTCTGCATTGCTGATGGCCTGGTTTGGTGTCCTGAGCTGTGTGCAG
GCCGAATTCTTCACCTCTATTGGGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTG
GTGCAGTCTCTGAAAGAGTACATCCTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGC
TGGGCCAACAAAATGGAAGCCTTGACTAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTG
GCTCACCCTGTGAATGCCTACAAACTGGTGAAGCGGCTAAACACAGACTGGCCTGCGCTG
GAGGACCTTGTCCTGCAGGACTCAGCTGCAGGTTTTATCGCCAACCTCTCTGTGCAGCGG
CAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAAAGCCCTGATGAGACTTCAG
GACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAACTTCCAGGAACCAAGTAC
CAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGCCTACAATGAAGGG
GACTATTATCATACGGTGTTGTGGATGGAGCAGGTGCTAAAGCAGCTTGATGCCGGGGAG
GAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTTCCAGTTG
GGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCTGCTCTCCCTTGACCCAAGCCAC
GAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAAA
ACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCATCTATGAGAGGCCT
GTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCGTGGGGAGGGTGTCAAA
CTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAACAGGGCCCCA
CAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGG
TACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAA
CTTGCACGAGCCACCGTTCGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTACCGG
GTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATCGT
CGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGC
GGCCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAA
GCTGGTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACA
GCTGTGTTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCT
GCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGA
CAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCCTTC
CCCTTCCTGGTCCTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCTTTGTAT
GTTCCTATCAGGCTGATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATA
CTAGGGCGACTCCTGTGTGACTGAAGTCCCAGCCCTTCCATTCAGCCTGTGCCATCCCTG
GCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGT
GCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACC
TTGTTTACATGTTTGTTTTTATGGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAA
TGTCCCTACCAGAAAAAAAAAA

FIGURE 116

><signal peptide>

MKLWVSALLMAWFGVLS

><start mature protein>

CVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWANKMEALTSKSAADAE

GYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIA

><N-glycosylation site.>

NLSVQRQFFPTDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCF

GMGRSAYNEGDYYHTVLWMEQVLKQLDAGEEATTTKSQVLDY

><potential Leucine zipper 213-234>

LSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLRYFEQLLEEEREKTLT

><N-glycosylation site.>

NQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRRQKRLFCRYHHGNRAP

QLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTGVLTVAS

YRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS

RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRS

GEGDYRTRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAG
TGAAATTGATTGTTTCATTTATTACCGTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGT
TGAAGAGCAGGCAGAAGGAGTTGTGAAGACAGGACAATCTTCTTGGGGATGCTGGTCCTGGA
AGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCCCAGGTTCTCTGGTTAAAACTGAA
AGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCCCCTGGGGCAC
CCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGC
TTCCCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGCGGGTTTCCTGGATC
CAGGGGGAGGGAGAAGATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCC
AGATTCGAGAGCTCGGCTAGACCAAAGTGATGAAGACTTCAAACCCCGGATTGTCCCCTACT
ACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTCGGTACATCCAGACAGAGCTG
GGCTCCCGTGAGCGGTTGCTGGTGGCTGTCCTGACCTCCCGAGCTACACTGTCCACTTTGGC
CGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGC
GGGGGGCCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGG
CTCATGTCAGAGACCCTGCGCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTT
CATCATGCAGGATGACACATATGTGCAGGCCCCCCGCCTGGCAGCCCTTGCTGGCCACCTCA
GCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTCATTGGCGCAGGCGAGCAGGCC
CGGTACTGTCATGGGGGCTTTGGCTACCTGTTGTCACGGAGTCTCCTGCTTCGTCTGCGGCC
ACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCCTGACGAGTGGCTTGGACGCT
GCCTCATTGACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCA
TTTGAACTGGCCAAAAATAGGGACCCTGAGAAGGAAGGGAGCTCGGCTTTCCTGAGTGCCTT
CGCCGTGCACCCTGTCTCCGAAGGTACCCTCATGTACCGGCTCCACAAACGCTTCAGCGCTC
TGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACTGCAGGCTCAGATCCGGAACCTGACC
GTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCAC
ACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCT
GTGCAGATGGGGCTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCG
TTGGAGACTGCCCTGGAGCAGCTCAATCGGCGCTATCAGCCCCGCCTGCGCTTCCAGAAGCA
GCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCACGGGGCATGGAGTACACCCTGGACC
TGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCAGGGTCAGCCTG
CTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGT
GCAGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCCTCGAGGCGT
TTGCAGCCAATGTCCTGGAGCCACGAGAACATGCATTGCTCACCCTGTTGCTGGTCTACGGG
CCACGAGAAGGTGGCCGTGGAGCTCCAGACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGA
GTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCGCTGTGCGAGCAGAGGCCCCTT
CCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCTGTGGACACTCTCTTCTTCCTT
ACCACCGTGTGGACAAGGCCTGGGCCCGAAGTCCTCAACCGCTGTCGCATGAATGCCATCTC
TGGCTGGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCACCACAGA
GATCACCCCCAGGGCCCCCGGGGGCTGGCCCTGACCCCCCCTCCCCTCCTGGTGCTGACCCC
TCCCGGGGGGCTCCTATAGGGGGGAGATTTGACCGGCAGGCTTCTGCGGAGGGCTGCTTCTA
CAACGCTGACTACCTGGCGGCCCGAGCCCGGCTGGCAGGTGAACTGGCAGGCCAGGAAGAGG
AGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCCTCCGGTTCTCAGGGCTCCACCTC
TTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCT
CAGTGAAGAACTCTACCACCGCTGCCGCCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCC
AGCTGGCTATGGCTCTCTTTGAGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGGCCC
TAACCTCATTACCTTTCCTTTGTCTGCCTCAGCCCCAGGAAGGGCAAGGCAAGATGGTGGAC
AGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAAACATGTCTTCTGCC

FIGURE 118

><signal peptide>
MRLSSLLALLRPALP
><start mature protein>
LILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDFKPRIVPY
YRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAV
><potential N-glycosylation site>
NRTVAHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYD
><homology to radical fringe -177-241>
WFFIMQDDTYVQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLR
LRPHLDGCRGDILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFL
SAFAVHPVSEGTLMYRLHKRFSALELERAYSEIEQLQAQIR
><potential N-glycosylation site>
NLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLGWDYFTEQHTFSCADGAPKCPLQGASRADV
GDALETALEQLNRRYQPRLRFQKQRLLNGYRRFDPARGMEYTLDLLLECVTQRGHRRALARR
VSLLRPLSRVEILPMPYVTEATRVQLVLPLLVAEAAAAPAFLEAFAANVLEPREHALLTLLL
VYGPREGGRGAPDPFLGVKAAAAELERRYPGTRLAWLAVRAEAPSQVRLMDVVSKKHPVDTL
FFLTTVWTRPGPEVLNRCRMNAISGWQAFFPVHFQEFNPALSPQRSPPGPPGAGPDPPSPPG
ADPSRGAPIGGRFDRQASAEGCFYNADYLAARARLAVNWQARKRRKPLEGLEVMDVFLRFSG
LHLFRAVEPGLVQKFSLRDCSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAAAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACTACATATCCAA
TACAGCTGTATGTTTCTTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTAAATGAGGGTGGTTTTTTTCTTTAAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTTGCTGATTGGTT
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

><signal peptide>

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHG

><start mature protein>

NRMHHHEHHHLQAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKETW

TKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDKYRDQYNWFFLARP

TTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGGIVLSVESMKRLNSLLNIP

EKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT

YHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFLPP

><potential N-glycosylation site>

NGSDND

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAAATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAATAAGTAGTTTTAAATGTTAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAA